035811 rattus norv 035786 rattus norv 099788 homo sapien 091977 mus musculu 098907 gallus gall 09wv08 mus musculu 063645 rattus norv 093361 meleagris g

rattus norv mus musculu mus muscalu

P55086

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINE-20459128; PubMed-10851239;

MEDINE-20459128; PubMed-10851239;

Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R., Willians D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N., Millians D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N., Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M., Lynch K.R., Evans J.P.;

"Characterization of the human cysteinyl leukotriene 2 receptor.";

J. Biol. Chem. 275:30531-30536(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-Placenta;
TISSUB-20344465; pubMed=10913337;
Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T., Nishikawa I., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321)
(hGPCR21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The molecular characterization and tissue distribution of the human cysteinyl leukotriene CysLT2 receptor.";
Biochem. Blophys. Res. Commun. 274:316-322(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Civelli 0.; "Molecular cloning and characterization of a second human cysteinyl leukotriene receptor: discovery of a subtype selective agonist."; Mol. Pharmacol. 58:1601-1608(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suga H.;
"Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
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SEQUENCE FROM N.A.
MEDLING=2054574P. PubMed=11093801;
Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                          346 A.A.
                                                                                                                                                                                                                   ALIGNMENTS
              P2Y6_RAT
P2Y4_RAT
P2Y4_RAT
CML1_RAT
CML1_BAY
P2Y4_MOUSE
P2Y3_CHICK
APJ_MOUSE
PARZ_RAT
CML1_MOUSE
PARZ_RAT
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Furuichi K.;
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Dunn M.
                                                                                                                                                                                                                                                               RESULT 1
CLT2_HUMAN
 A LO DE LO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meleagris
gallus gall
gallus gall
rattus norv
homo sapien
bos taurus
mus musculu
homo sapien
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mus musculu
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homo sapien
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homo sapien
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674.731 Million cell updates/sec
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P32250
P49651
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Compugen Ltd.
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                 GenCore version
Copyright (c) 1993 - 2003
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P2Y2_RAT
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P2YR_MELGA
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PAR1 XENLA
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 MEPNGTFSNNNSRNCTIENF.
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                                             197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 256
                                                                                                                                            FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
MINIAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136
                            FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                    181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata, Vertebrata, Buteleostomi, actyla, Suina, Suidae, Sus.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PRINTS; PRO153; CYCREHODOPSN.
PROSITE; PS00337; GPROTEIN RECEP_FI_2; I.
PROSITE; PS50262; G_PROTEIN_ERCEP_FI_2; I.
G-protein coupled receptor; Transmembrane; Glycopridomain: 43 EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
receptor 2 (CysLTR2).
                                                                                                                                                                                                        KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                                                                                                                       317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
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Interpro; IPR004071; Cysleuk_receptor.
Interpro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 CYSLTR2 OR CYSLT2.
                                                                                                                                                                                                                                                                                                                                                                                                                   (Pig)
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                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MINLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 MEPUGTESNNNSFNCTIENFKREFFIVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEPNGIFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
            FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-Protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is IIC4 = IID4 >> IIP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.

TISSIB SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, splean, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.
                                                                                                                                                                                         SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CTIOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CTIOPLASMIC (POTENTIAL).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 142 EXTRACELIDIAR (POTENTIAL).
(APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELIULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004974; F:leukotriene receptor activity; NAS. GO; GO:0030105; F:nanaphylaxis, NAS. Interpro; IPR004071; Cysleuk_receptor. Interpro; IPR000276; GPCR_Rhodpsn.
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EMBL; AP254664, AAG17281.1; --
EMBL; AP279611; AAK59485.1; --
EMBL, AL137118; CAC29102.1; --
EMBL; AB083603; BAB839316.1; --
EMBL; AB041644; BAB16379.1; --
Genew; HGWC:18274; CYSLTR2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                     EMBL, AP331658; AAK97354.1; -. MGD: WGI:1917336; Cysltt2.
MGD: WGI:001631; F:cysteinyl leukotriene receptor activity; IDA.
INTERPRO; IPR004071; Cyslauk, receptor.
InterPro; IPR004071; GFCR_Rhodpsn.
                                                                                                                                                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Indels
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                             FFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDR 299
                                                                                                                                                                                                                             1 MEPNGIFSNNNS-RNCTIENFKREFFPİYYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNV 59
                                                                                                                                                                                                                                              1. Biol. Chem. 276.47489-47495(2001).

1. FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.

1. SUBCELLULAR LOCATION: Integral membrane protein.

1. TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.

1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                         BY STAILARITY.

N-LINKED (GLONAC. ) (POTENTIAL).

N-LINKED (GLONAC. ) (POTENTIAL).

N-LINKED (GLONAC. ) (POTENTIAL).

N-LINKED (GLONAC. ) (POTENTIAL).

5 DIBIFB89B895905 CRC64;
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                                                                                                                                                                                                  3;
                                                                                                                                                                  Score 1367.5; DB 1; Length 345; Pred. No. 7.9e-78;
                                                                                                                                                                                                  42; Indels
               EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 LKSALRKGRPQ--KTRCGFSVCVWLKKETRV 345
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                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                24;
                                                                                                                                     39410 MW;
                                                                                                                                                                   79.98;
79.28;
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267
287
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                                                                                                                                     345 AA;
                                                                                                                                                                                  Similarity
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CYSLTR2 OR CYSLT2
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Matches 262;
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                                                          DISULFID
                                                                                                       CARBOHYD
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               241 FLCFLPYHTLRTVHLTTWKYGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i-FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0237; CYSTIRECPTR.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1).
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InterPro; IRR040471; Cysleuk_receptor.
InterPro; IRR0000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         (Rat).
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Q924T8;
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                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute; There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
                                                                                                                                                               Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                     receptors.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By Similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR004071; Cysleuk receptor.
PINTER: PR001513; CYSLTRECPTR.
PRINTS; PR001533; CYSLTRECPTR.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DOMAIN
TRANSMEM 27 47; (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1187; DB 1; Length 309;
Pred. No, 9.3e-67;
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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A122AC$177879D56 CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2) (RSBPT32).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
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26; Mismatches
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Best Local Similarity 73.1
Matches 225; Conservative
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166
167
309 AA;
                                    CYSLIR2 OR CYSLIZ.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID=10116;
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InterPro; IPR000276; GPCR_Rhodpsn
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                                                                                                                                                                                                                                                                                                                                                                                                                     HPFRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--L 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFLPYHILRIVHL--TIWKVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes mediating
construction of the microvascular smooth muscle during an
inflammatory response. This response is mediated via a G-protein
that activates a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system (By similarity).
SUBCELLUIAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Buteleostomi, etyla; Suina, Suidae, Sus.
                   BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                       25;
                                                                                                                                    Score 567.5; DB 1; Length 339; Pred. No. 1.4e-28;
                                                                                                                                                                                       70; Mismatches 115; Indels
    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 1 (Cyslfrl).
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLKSALRK------GHPQKAKTKC 316
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Mammalia, Butheria, Cetartiodactyla,
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                                                                                              39143 MW;
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                                                                     171
                                                                                              339 AA;
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DOMAIN
DISULFID
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                                                CARBOHYD
                                                                        CARBOHYD
                                                                                                SEQUENCE
                                                                                                                                         Query Match
Best Local S
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CLT1_PIG
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EMBL; AB052686; BAB60826.1; -. InterPro; IPR004071; Cysleuk_receptor.

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68 DILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 FRLIHVTSIRSAWILCGIIWI-LIMASSIMILDSGSEQNGSVTSCLELNLYKIAK--LQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 SNNNSRNCTIENFKREFFFLVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVFMLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF
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CITI_MOUSE STANDARD;
099JA4; 09JXT47;
28-FEB-2003 (Rel. 41, Careated)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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PRINTS; PRO1533; CÏSLTRECPTR.
PRINTS; PR00237; GPREHDOPSN.
PROSTER; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN
32 1 (POTENTIAL).
TRANSMEM 32 52 I (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                 3 (POIENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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265 N
38986 MW;
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                                                                     Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.; Infontification in mice of two isoforms of the cysteinyl leukotriene lareceptor that result from alternative splicing."; Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISOIG-090774-7; Sequence-VSP_001921; TISOIG-090774-7; Sequence-VSP_001921; TISOIG-090774-7; Sequence-VSP_001921; TISOIG-090774-7; Sequence-VSP_001921; TISOIG SPECIFICITY: Widely expressed, with higher expression in the heart, kidney and stomach and lower levels in several other tissues. Isoform 1 is the most abundant form in all tested tissues. AMSCELLANBOUS: MK-571, a selective antagonist, was shown to inhibit eosinophilla, bronchial hyperreactivity and microvascular leakage. Zafirlikast (Accolate) and pranlukast (Onon) were also shown to be selective antagonists. SIMILANITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-6275TM/6, TRSOBE-TRACHEN,
MEDLINE-21562332; PubMed-T1105452;
Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. It is response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 >> LTB4 = LTG4 >> LTB4.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
-!- Brent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.; "Identification of a murine cysteinyl leukotriene receptor by
                                                                                                                                                                                                                                                                                                                      "Molecular cloning and functional characterization of murine cysteinyl-leukotriene 1 (CysLT1) receptors.";
Biochem. Pharmacol. 62:1193-1200(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression in Xenopus laevis oocytes.";
Biochim. Biophys. Acta 1517:455-459(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=Long;
IsoId=Q99JA4-1; Sequence=Displayed;
Name=2; Synonyms=Short;
FROM N.A. (ISOFORMS 1 AND 2).
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MEDLINE=21240338; PubMed=11342226;
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                                                PubMed=11226226;
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                        STRAIN=129/Sv;
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246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLKS 302
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 2).
XISAING (in Isoform 2).
X -> D (IN REF. 3).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLFR1) (Cysteinyl leukotriene receptor) (LTD4 receptor) (HG55) (HWIMFR1).
CYSLFR1 OR CYSLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Mismatches 108; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%; Score 560; DB 1; Length 352; 38.5%; Pred. No. 4.1e-28;
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG. PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Alternative splicing.
                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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5BDC94B3F1CD0CAB CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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40715 MW;
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                                                                         Similarity
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Q9Y271;
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Query Match
Best Local Simi
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R GO; GO:000524; C:membrane fraction; TAS.

R GO; GO:000524; E:membrane fraction; TAS.

R GO; GO:0005204; F:lewthotriene receptor activity; TAS.

R GO; GO:0007204; P:lewthotriene receptor activity; TAS.

R GO; GO:0007204; P:lewthotriene response; TAS.

R GO; GO:00075204; P:lewthotriene response; TAS.

InterPro; IPR00477; Cysleuk_receptor.

R FinterPro; IPR00477; Cysleuk_receptor.

R PROFIT: PR00027; GPCRHODOPSN.

R PRNTS; PR001533; GPCRHODOPSN.

R PROSITE; PS00237; GPROTEIN_RECEP_FI_1; FALSE_NEG.

R PROSITE; PS00237; GPROTEIN_RECEP_FI_2;

R PROSITE; PS00237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Leukocyte, Peripheral blood monocytes, and Spleen, MEDLINE-9939629; PubMed=10462554; Asara H.M. Ames R.S., Chambers J., Elis C., Elshourbagy N., Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P., Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor."; Mol. Pharmacol. 56:657-663(1999).
                                                                                                                                                                   Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M., Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M., Bai C., Austin C.P., Chateauneuf A., Stocco R., Greig G.M., Kargman S., Hooks S.B., Hofsfield E., Williams D.L. Jr., Ford-Hutchinson A.W., Caskey C.T., Evans J.F., "Characterization of the human cysteinyl leukotriene CysLrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.

SIMILARITY: BELONGS TO PAMILK 1 OF G-PROTEIN COUPLED RECEPTORS.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                             MEDLINE=99318129; PubMed=10391245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399:789-793(1999).
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    [1]
SEQUENCE FROM N.A.
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129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
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MEDLINE=98181695; PubMed=9523551;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
"A novel orphan G protein-coupled receptor primarily expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 NYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL
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MEDLINE-96145150. Pubmed-8558062;
RAPORT C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.
Godiska R., Gray P.W.;
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Mammalia; Butheria; Prlmates; Catarrhini; Hominidae; Homo.
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""LINKED (GLCNAC. .) (POTENTIAL).

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""LINKED (GLCNAC. .) (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable P2Y purinoceptor GPR17 (P2Y-like receptor) (R12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106; Indels
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                              CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 559; DB 1; 38.0%; Pred. No. 4.5e-28; tive 71; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 AA.
                                        (POTENTIAL)
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38541 MW;
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262
337 AA;
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                                              163 HPVKSIKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 219
                                                                                                      220 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 273
                                                                                                                                                                 HPFRILHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                242 LCFLPYHTLRTVHLITWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALTIIITLIIFF
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Archosauria, Aves, Neognathae, Galliformes, Meleagrididae, Meleagris.
NCBL_TaxID=9103;
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MEDLINES-9738246; PubMed=9240460;

Li O., Schachter J.B., Harden T.K., Nicholas R.A.;

The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not mediate nucleotide-promoted second messenger responses.";

Blochem. Blophys. Res. Commun. 236.455-460(1997)

-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADDENINE NUCLEOTIDES SUCH AS ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERFUSSIS TOXIN INSENSITYEE A PROFIBIN. PROBABLY BELONGING TO THE GO FAMILY THAT ACTIVATE A PROFIBININISTICL—CALCING SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2X purinoceptor 1 (ATP receptor) (P2X1) (Purinergic receptor) (6H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDINE-9435507; PubMed-8058061;
Filtz T.M. Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
"Expression of a cloned P2Y purinergic receptor that couples to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0237; GPCRRHODOPSN.
PROSTIE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS050262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS050262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                               362 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meleagris gallopavo (Common turkey).
                                                                                                                                                                                                              DRLKSAL ---- RKGHPQKAKTK 315
                                                                                                                                                                                                                                               334 HALCNLLCGKRLKGPPPSFEGK 355
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmacol. 46:8-14(1994).
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                                                                                                                                                                                                                                                                                                                                 STANDARD;
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P49652;
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                 126
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GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0007186; F:Grotein coupled receptor protein signalin. . .; TAS.
InterPro; IRR000276; GPCR_Rhodpsn.
Pfam. PF00001; 7tm_1; 1.
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brain is localized on human chromosomal band 2q21.";
J. Neurochem, 70:1357-1365(1998).
-!- FUNCTION: Putative receptor for purines coupled to G-proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                          "Isoid-013304-2; sequence-vsp_001987;
!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.
!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

N-LINKED (GLONAC. ) (POTENTIAL).

N-LINKED (GLONAC. . ) (POTENTIAL).

N-LINKED (GLONAC. . ) (POTENTIAL).

Missing (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 4.1e-23;
62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G-PROTEIN RECEP_F1_7; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                 Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSP_001987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
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                                                                                                                              IsoId=Q13304-1; Sequence=Displayed;
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EMBL; Y12546; CAA73144.1; -.
EMBL; 294154; CAB08107.1; -.
EMBL; Z94155; CAB08108.1; -.
HSSP; P34996; IDDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40989 MW;
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hes 112; Conserv
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                                                                                                                  Name=1
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MEDLINE-97026378; PubMed-8872457;

Van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;

van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;

van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;

van Modelling the P27 purinoceptor using rhodopsin as template.";

Drug Des. Discov. 13:133-140(1995).

-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS

ATP AND ADD. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN

INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GO FAMILY THAY

ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFCITY: BRAIN, SPINAL CORD, GASTROINFESTINAL TRACT,

SPLERM AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
                                                                                                                                                                                                                                                                  PIR; S33733; S33733.
PDB; 1DDD; 11-JUL-96.
InterPro; IPR000276; GPCR_Rhodpsn.
324:219-225(1993).
                                                                                                                                                                                                                                                        EMBL; X73268; CAA51716.1; -.
                                                                                                                                             LUNG AND KIDNEY
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317
362
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                    3D-STRUCTURE MODELING
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98; Conserv
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Matches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  IITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                           GWAAGNASTKCSLIKTGFQFYYLPTVYILVFITGFLGNSVALWMFVFHMRPWSGISVYMF 80
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                                                                                                                                                                                                                                                                    GTFSNNNSRNCTI -- ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Meognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-93225340; PubMed-8508924; MEDD T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G., King B.F., Burnstock G., Barnard E.A.; "Cloning and functional expression of a brain G-protein-coupled ATP
                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEB-1994 (Rel. 28, Created)
FEB-1994 (Rel. 28, Last sequence update)
FEB-2003 (Rel. 41, Last annotation update)
purlinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                          Length 362;
                                                                                                                                                                                                                    27.5%; Score 470; DB 1; Lengua ...
31.0%; Pred. No. 1.4e-22;
" Wismatches 112; Indels
                                                                                  EXTRACELLULAR (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
                                                                                                                        EXTRACELLULAR (POTENTIAL) 7 (POTENTIAL).
                                                                                                                                                                                              LINKED (GLCNAC. . .) (POSEL28AB9EB64349C CRC64;
                                         EXTRACELLULAR (POTENTIAL)
         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                             CYTOPLASMIC (POTENTIAL).
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                                (POTENTIAL).
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CYTOPLASMIC (
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 1156
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362 AA;
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es 99; Conserv
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28-FEB-2003
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P34996;
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                                                                                                                                                                                                                                                                                                                                                                                     InterPro; Lravou...;
Pfam, PF00001; 7tm_1, 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-PROTEIN COUPLED receptor; Transmembrane; Glycoprotein; 3D-structure.

4. EXTRRCELLUIAR (POTENTIAL).
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LHVISIRSAWILCGIIWILIMASSI----MLLDSGSRQNGSVTSCLELNLYKIAKLQTMNY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAL---VVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 211:211-218(1995).
-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADSMINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS OF EXTRACELLULAR ATP ON INNSULIN SECRETION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISONE SPECIFICITY: EXPRESSED IN MISCLE, HEART, LIVER, KIDNEY, LIVE, BRAIN, SPLEEN, BUT NOT IN TESTIS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVALYIFTFTLKVRNETTTYMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 LPYH-----TLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                    EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (TOTENTIAL).
N-LINKED (GLONAC. . . ) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2X1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Insulinoma;
MEDLINE-95298025; PubMed=7779087;
Toknyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
"Cloning of rat and mouse P2Y purinoceptors.";
                                                                                                                                                                                                                                                  POTENTIAL.
4214E969633B6F7D CRC64;
                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                      53; Mismatches 119;
                                                                                                                                                                                                                                                                                                                             Score 447; DB 1;
Pred. No. 3.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 AA
                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                         35597 MW;
                                                                                                                                                                                                                                                                                                                               26.1%;
35.4%;
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 35.4 es 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
178
2206
2224
2250
2269
308
308
5
                                                                                                                                                                                                                                                                         308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                        281
                                                      DOMAIN
TRANSMEM
                                                                                                       DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P2YR_RAT
                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                         SEQUENCE
                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                  Query Match
  DOMAIN
                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
P2YR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P2RY1
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÓΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \delta \Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               |||::||::|||:|||:||||::|||||::|:||||::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
                                                                                                             173
                                                                                                                                                                                                                                                                                                                               287
NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
                                                                                                                                                                                                                     LNLYKIAKLQTMNYIALVYGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
                                                                                                                                                                                                                                                                      LRSYFVYSMCTTVFMFCI -- -- PFIVILGCYGLIVKALIYKDLDNSPLR---RKSIYLV 251
                                                                                                                                                                                                                                                                                                                                                                              IIVLTVFAVSYLPFHVMKTLNLRARIDEQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311
                                                                                                                                             123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----
                                                                                                                                                                                                                                                                                                                             IITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAANACFNPL
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Pfam; PF00001; 7tm_1; 1.
PRTMTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Iransmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaplan M.H., Smith D.I., Sundick R.S.; "Identification of a G protein coupled receptor induced in activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2x purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENITAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93329058; PubMed-8393036;
                                                                                                                                                                                                                                                                                                                                                                                                                                       LYYFAGENFKDRLKSALRK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: ||: |: || | ||
LYFLAGDTFRRLSRATRK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunol. 151:628-636(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L06109; AAB06587.1; -. PIR; I50241; I50241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
43
52
76
89
109
130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
53
77
90
110
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TRANSMEM
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DOMAIN
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TRANSMEM
                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                252
                                                                                                                                                                                                                                                                                                                                                                                                                                       288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
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                                                      81
                                                                                                                                                                                                                                                                                                                             234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
P2Y5_CHICK
ID P2Y5_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P2RY5
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purinoceptor.
                                                                                               purinoceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 601167;
                                                                                 Kunapuli S.P.
                                                                                                                                                                           TISSUE=Blood;
                                                                                                                                                      Biochem.
  9
                                                                                                                                                                                                                                                                                                                       211
                                                                                                                                                                                                                                                                                     ITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHRALVITLALAAANACFNPLL 288
                                                                                                                                                                                                                                                                                                                                                                         LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
                                                                                                                                                                                                                                                                                                        124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE----L 174
                                                                                                                                                                                                                                                                                                                                     175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTII 234
                                                                                                                                                                                                                                                        6 TFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                                                                                                                                                                                                                                                                                                                  26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEE-1996 (Rel. 33, Created)
FEE-1996 (Rel. 33, Last sequence update)
FEE-2003 (Rel. 41, Last annotation update)
Purinoceptor 1 (ATP receptor) (R2X1) (Purinergic receptor)
                                                                                                                                                                                                                   26.1%; Score 447; DB 1; Length 373; 32.1%; Pred. No. 3.8e-21;
  81; Mismatches 109; Indels
                                                                               2 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                             EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                      6DDF676287B5E648 CRC64;
                                                                1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                            3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AA.
                                                                                                                         (POTENTIAL).
                                                                                                                                                     (POTENTIAL).
                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     YYFAGENFKDRLKSALRK 306
                                                                                                                                                                                                    42321 MW;
EMBL; U22830; AAA91303.1;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                               109
126
147
166
                                                                                                                                                                                       113
197
373 AA;
                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
                                                                                                                                                                                                                                 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                              P2YR_HUMAN
P47900;
                                                                                                  DOMAIN
TRANSMEM
DOMAIN
                                                                                    DOMAIN
TRANSMEM
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                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                            DOMAIN
DISULFID
                                                                                                                                                                                              CARBOHYD
SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSTITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
PROSTITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
TISSUE-Placenta;
MEDLINE-96257237; PubMed-8666290;
Leon C., Vial C., Cazenave J.-P., Gachet C.;
"Cloning and sequencing of a human cDNA encoding endothelial P2Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96205320; PubMed=8630005;
Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and tissue distribution of the human P2X1 receptor."; Biophys. Res. Commun. 221:588-593(1996).
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GO; GO:00004872; F:receptor activity; TAS.
GO; GO:00007200; F:G-protein signaling, coupled to IP3 second
InterPro; IPR000776; GPCR_Rhodpsn.
PF000011; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and chromosomal localization of the human P2Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 218:783-788(1996).
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EMBL, U42030; AAA97873.1; --
EMBL, U42029; AAA97872.1; --
EMBL, S81950; AAB47091.1; --
EMBL, AJ006945; CAA07339.1; --
FMBL, AJ018245; CAA07339.1; --
FMBL, AJ04737; J04737; HSSP; P34996; IDDD.
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                                                                                                                                                                                                                                                                                           Gene 171:295-297(1996).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----LNLYKIAKLQTMN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corpus callosum.";
Neurobiol. Dis. 5:259-270(1998).
-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                            Miledi R.; from the adult bovine
                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Integral membrane protein.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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PRINTS; PR00337; GPCRHRODOPSN.
PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN.

52 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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Source and (Potential).
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CYTOPLASMIC (POTENTIAL).
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 Commun. 212:648-656(1995).
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31.0%; Pred. No. 7.8e-21;
iive 78; Mismatches 109;
                             SEQUENCE FROM N.A.
TISSUE-Corpus callosum;
MEDLINE-99064562; PubMed-9848096;
MEDLINE-00. Kumar C.K., Pogarty D.J., I
"Cloning and expression of a P2y purinoceptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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Pfam; PF00001; 7tm_1; 1.
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 Res.
                                                                                                                                                                                                                                                                                                                                                                    JC4162,
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95; Conserva
 Biophys.
                                                                                                                                                    ATP AND ADP.
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   Biochem.
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Bukaryota, Metazoa; Chordata, Craniatà; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                       (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL).
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MEDLINE-95352058; PubMed-7626079;
Henderson D.J., Ellot D.G., Smith G.M., Webb T.E., Dainty I.A.;
"Cloning and characterisation of a bovine P2Y receptor.";
                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
PTER-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
P2Y purinoceptor 1 (APP receptor) (P2X1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                  Length 373;
                                                                                                                                                                                                                                                                                                                                                                                               111; Indels
                                                                                                         4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTAL')
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EXTRACELLULAR (POTENTIAL).
                EXTRACELLULAR (POTENTIAL).
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4DC7C668B4145392 CRC64;
                                                                            EXTRACELLULAR (POTENTIAL)
                                           CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                         3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                            (POTENTIAL).
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Pred. No. 4.4e-21;
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138
373 AA;
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3lood coagulation
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CARBOHYD
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REPERENCE OCCOS ON REPERT OCCOS OCCO

QY	247 YHTLETVHLTTWKVGLCKDRIHKALVITLALAAANACENPLIXYEAGENFKDRL 300
qq	276 FHVMKTMNLRARLDFQTPBMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
δž	301 KSALRK 306
qq	336 SRATRK 341
Search Job tim	Search completed: October 8, 2003, 08:28:46 Job time : 24 secs

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October 8, 2003, 08:26:59; Search time 97 Seconds (without alignments) 877.911 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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2: sp_archa:*
3: sp_fungi:*
4: sp_human:*
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7: sp_mnamal:*
8: sp_mammal:*
10: sp_plant:*
11: sp_plant:*
12: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q8r528 mus musculu Q8iv19 homo sapien Q96p68 homo sapien Q96b57 homo sapien Q96b57 homo sapien Q96x57 xenopus lae Q8bmc7 xenopus lae Q8bmc0 mus musculu Q8bmc0 mus musculu Q8bx1 mus musculu Q9by7 anguilla an Q9yy7 anguilla an Q9yy7 anguilla an Q9gyy7 sagilla anguilla
SUMMARIES	QRR528 Q91V19 Q96F68 Q90F57 Q90E05 Q90EX57 Q90EX57 Q8BEXC1 Q8BEXC1 Q8BEXC1 Q9EX77 Q9FVY7 Q9CV7 Q9GX76 Q9TV7 Q9GX76
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Result	114440000010004000

Q9dhv5 yaba-like d Q911y8 rattus norv Q9try6 canis famil Q8c131 mus musculu Q8brw4 mus musculu Q8brw4 mus musculu Q8bry18 callithrix Q8T311 mus musculu Q8bry1 mus musculu Q9bry2 xenopus lae Q9qq16 mus musculu Q9trx6 mccaca mula Q9try7 cercopithec Q9try7 cercopithec Q9try7 cercopithec Q9try7 cercopithec Q9try7 cercopithec Q9try7 cercopithec Q9try7 cercopithec Q9try7 orvoicagus Q9cxfs mus musculu Q8try8 mus musculu Q9try7 orroriosapien Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu Q9erx9 mus musculu	W	. AA .	e update) ion update)	raniata; Vertebrata; Buteleostomi; clurognathi; Muridae; Murinae; Mus.	EMBL/GenBank/DDBJ databases. odpsn. RECEP_F1_2; 1.	DB 11; e-90; 52;	MEPNGTPSNNCTIENEKREFPIVYLJIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60	MLNLAISDILFISTIPPRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVR 120 	
Q9DHV5 Q9JIY6 Q94IIY6 Q94IIY6 Q94II31 Q88YIQ8 Q9X78 Q9X78 Q9X78 Q9X78 Q9X78 Q9X76 Q9X10 Q911C0 ALIGNMENT	PRT; 309	Created) Last sequence Last annotatic	ပတ	e EMBL/GenBank/DDBJ ; Rhodpsn. N_RECEP_F1_2; 1.	ŠĢ.,	KREFFPIVYLI: : : : KKEFYPIIYLI	YYLRGSNWIFG! YYFRGSNWIFG!	ILCGIIWILIM	
211011144011114 210 21140 1140 1140 1140			21, Cr 21, La: 23, La: recept	Chordata; Rodentia;	the E 2.1; - 2. R_Rho EIN_R	; ; %	riene riene	PFRAD PFRAD	IRSAW
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8888 88 88 88 88 88 88 88 88 88 88 88 8		1 R528 R528;	-JUN-200 -JUN-200 -MAR-200 steinyl	Mus musculus (Mouse). Eukaryota, Metazoa, C. Mammalia, Eutheria, R. NCBL_TaxID=10090;	L11 Ishi S.; "Mouse Cysir2 Gene."; "Mouse Cysir2 Gene."; "Mouse Cysir2 Gene."; EMBL, ABO58930; BAB66681.1; MGD: MGT:1917336; Cysir2. Interpro; IPR000276; GPCR_Rhoc Pfam; PP00001; Tum_1; 1. PROSITE; PS50262; G_PROTEIN_RI Receptor.	Match Local Les 22	1 M	61 M 61 M	
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129 RLLHVTSIRSAWILCGIIWILIMASSI----MLLDSGSEQNGS----VTSCLELNLYKIAK 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 NCTDENIPLEXMETLEVITELINGEPGRAVVISTYIFKARPWKSST---IIMLNLACTD
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   receptor)
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PubMed=12098360;
Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.J.,
Schaller H.C., Hampe W.;
"GPR99, a new G protein-".coupled receptor belonging to a new subgroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human
                                                                                                                      Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               [1]
SECURICE FROM N.A.
SECURICE FROM N.A.
MEDLIKE-21458857; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko (
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
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coupled
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GPR99 (Putative G-protein
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ilarity 34.9%; Pred. No. 5.2e-32;
Conservative 64; Mismatches 114;
G protein-coupled receptor GPR99 (Pu (Seven transmembrane helix receptor) GPR80 OR GPCR OR GPR99.
                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                    Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMC Genomics 3:17-17(2002)
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                                                                                                                                129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLIDSGSEQNGSVTSCLEINLYKIAK--LQTM 185
FLCFLPYHTLRIVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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                                                                                               KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC035750; AAH35750.1; -.
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337 AA; 38486 MW; B9B09CEOFD305245 CRC64;
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Last annotation update)
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01-MAR-2003 (TIEMBLIEL. 23, Last sequence update)
01-MAR-2003 (TIEMBLIEL. 23, Last annotation update)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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84 YVFSLPILIFYYENKTDWIFGELLCKLXRRFIFHYNLYGSILFLTCISVHRYTGVVHPMKS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: | | :: :: | :: | | | :: | : | | :: | : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
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Xenopus laevis (African clawed frog).
Bukaryota; Metazoa: Chordata; Cranieta; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                           Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.T., Connolly G.C., Ballatori M., Boyer J.L., Nathanson M.H.;

"A primitive APP receptor from the little skate Raja erinacea.";

"J. Biol. Chem. 275:30701-30706(2000).

EMBIS. AR242850, AAG42684.1;

PRIMITS, PROJOZ76; GPCR_Rhodpsn.

PRAMTS, PROJOZ75; GPCR_Rhodpsn.

PROSITE; PSOO237; GPROMENN.RECEP FIL!;

PROSITE; PSOO237; GPROTEIN.RECEP FIL!;

PROSITE; PSOO262; G_PROTEIN_RECEP_FIL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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"Cloning of Xenopus P2Y1 Receptor.";

"Cloning of Xenopus P2Y1 Receptor.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF42354; ABL2764.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Prim: PF00001; 7tm_1: 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPROTEIN_RECBP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECBP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AA; 41002 MW; E5B2D605F5B57FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               357 AA; 41239 MW; 14604EE15DCBDB41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TIEMELRE1. 19, Created)
01-DEC-2001 (TIEMELRE1. 19, Last sequence update)
01-MAR-2003 (TIEMELRE1. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 457; DB 13;
29.0%; Pred. No. 1.7e-29;
iive 87; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 TFRRETINAASREMIRRSELSMQFRSEDSPLQPVS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 NPKDRLKSALRKGHPQKAKTKCVF-----PVS 321
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                                                                                  MEDLINE=20459151; PubMed=10900200;
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NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 MNYIALVVGCLLPFFILSICYLLIIRVILKVEVPESGLRVSHR---KALTIIITLIIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoldea;
Rajiformes; Rajidae; Raja.
NCBL_TaxID=7782;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSURE-BEAIN, and Lung; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA; 37860 MW; BBOCAFDOFC371D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TIEMBLE1 22, Last sequence update) 01-MAR-2003 (TIEMBLE1 23, Last annotation update) G protein-coupled receptor 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 477; DB 4;
34.8%; Pred. No. 3.8e-31;
iive 61; Mismatches 127,
                                                                                                                                                                                                                    339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRNUTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPPOTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
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                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRLKSAL ----RKGHPQKAKTK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23, 1)
   RLKSALR --- KGHPQKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 34.8%;
Matches 112; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
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299
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III
RX SEQUENCE FROM N.A.
RX MEDLINE-22354683; PubMed-12466851;
RX The FRANCM COnsortium.
RA The FRANCM Consortium.
RA The FRANCM Consortium.
RA The RANCM Consortium.
RA The RANCM Consortium.
RA The RANCM Consortium.
RY G0.770 tull-length colbs.
RI G0.770 tull-length colbs.
RI Nature 420.563-573(2002).
DR EMBL; AK032901; BAC28077.1; -
SEQUENCE 344 AA; 39438 MM; 50270DID14AEDAB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 FRLLHVTSIRSAWILCGIIWILIM---ASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALV-----ITLALAAANACFNPLLYYFA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 CFCFVPIN----INLILYSLARTQTFVNCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFT 294
        ---TTWKVGLCKDRLHKALVITLALAAANACFNPIL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 DLLFVFTLPFRI-FYFATRNWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNNNSRNCTIENFKREFFPIVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVFMLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 -MNYIAL---VVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  PIT purinoceptor 5.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.5%; Score 436.5; DB 11; Length 32.4%; Pred. No. 7.7e-28; ive 72; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                         344 AA.
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                                                                                                                                                                                                                                                                                           PRT;
          ITLIIFFLCFLPYHTLRTVHL--
                                                                                                                                         289 YYFAGENFKDRLKSALRK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23,
23,
                                                                                                                                                                                                                                                                                                                                       Local Similarity 32.49
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 GENFKDRLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P2Y purinoceptor 9.
Mus musculus (Mouse).
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 LITFELCELPYHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLLYY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| : :||:| :: |:| ||: :| ||: ||:| ||: ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYHPFRLLHVISIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----L 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTII 234
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                                                                                                                                                                                                                                                                                                                 HPPRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----LNL 176
                                                                                                                                                                                                                                                                                                                                                                    143 HPLKSLGRLKKKNSIYISALVWFIVIAGISPILFFSGTGIRKNKTIT-CFDTSSDEYLKS 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 IAAVSSSFQCALIKIGFQFYYLPAVYILVFIIGFIGNSVAIWMYVFHMKPWSGISVYMFN 92
                                                                                                                                         The FANTOM Consortium,

The RIANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

#ANDLOS 63-75(2002).

BMBL; AR 201563-75(2002).

BMBL; AR 201563-75 BAC27125.1;

SEQUENCE 373 AA, 42228 MW; BA88124B7847287C CRC64;
                                                                                                            8 SNNNSRNCTI -- ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                        YKIAKLQIMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIIT
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P2Y purinoceptor 1.
Mus musculus (Mouse).
Eukarmyota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
     Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Mismatches 111; Indels
                                                           114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%; Score 439; DB 11; 30.5%; Pred. No. 5.2e-28;
        DB 13;
                                   3.68-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA.
                                                              Mismatches
          Score 453;
                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
                                                        80;
  26.5%;
30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 FAGENFKDRLKSALRK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 LAGDTFRKLSRATRK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23,
                                                              96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel, 01-MAR-2003 (TrEMBLrel, 01-MAR-2003 (TrEMBLrel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 97; Conserv
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8BMJ5;
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                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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us-09-991-225-2.rspt

SOR REPRESENTATION ON SOR REPRESENTATION OF

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APPLIANCE FROM N.A.
RX STRAIN=C57BL/6651;
RX MEDLINE=2334683, PubMed=12466851;
RA The FANTOM Consortium,
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of RT *Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-length cDMAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK045289; BAC32299.1;
SEQUENCE 370 AA; 41872 MW; 0E4C79FEDFD32050 CRC64;
                                                                                                                                             78 RADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIR 137
                                                                                                                                                                     138 SAWILCGIIWILI --- MASSIMLIDSGSEQNGSV --- TSCLEINLYKIAKLQTWNYIAL 190
                                                                                                                                                                                                                                                                                                                   247 YHTLRTVHLTT-WKVGLCK--DRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSA 303
                                                                                                                                                                                                                                                                                                                                                                                          64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 -LQTMNYIALVVGCLLPFFTLSICYLLIIRVILKVEVPESGLRVSHRKALFTIIITLIIF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FLCFLPYHTLRTVHLFTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGSEQNGSVTSCLELNLYKIAK- 181
                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 GNATANNT -- CIVDDSFKYNLNGAVYSVVFILGLITSSASLFVFCFRMKMRSETAIFIIN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GIPSNNNSRNCTI-ENFKREFFPIVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                                                                                                                                                                                                                                                37 EEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTYMFNLAISDTLYVFSLPT
                                                                    18 ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPF
                                                                                                                                                                                                                                                                                             191 VVGCL--LPFFTLSICYLLIIRVLLKVEVPESGLRV-SHRK-ALTTIITLIIFFLCFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P2r purinoceptor 9.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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Last annotation update)
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7; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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31.0%; Pic.
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23,
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:| |: :
LRRGAAQRPR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                             304 LRKGHPQKAK 313
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                               δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                           124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-IDSGSEQNGSVTSCLELNLYKIAK- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                             STRAIN-C57BL/61; TISSUE-Dorsal root ganglion;
MEDLINE-2234683: PubMed=12466851;
The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
thanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length DDMas.";
Nature 420:563-573(2002).
EMBL; AKUSI709; BAG347291;
SEQUENCE 370 AA; 41956 MW; AB126B42343AE6EI CRC64;
                                                                                                                                                                                                                                                                                                                           5 GTFSNNNSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIXVFLQPYKKSTSVNVFMLN
                                                                                                                                                                                                                                                                                                                                                    64 LAISDILFISTLPFRADYVLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 -LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 YLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLSQIGTNKKKVLKMITVHMAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
NCBL_TaxID=9103;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an avian G protein-coupled P2Y
                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                      ; Score 425; DB 11; Length 370;
; Pred. No. 7.1e-27;
68; Mismatches 134; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        849C465722BDD02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 424.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein coupled P2Y nucleotide receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KD-----RLKSALRKGHPQKAK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boyer J.L., Waldo G.L., Harden T.K.; "Molecular cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meleagris gallopavo (Common turkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Pharmacol. 52:928-934(1997).
EMERI, AR031897; AAC60339-11, -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF000001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Blood;
MEDLINE-98086419; PubMed-9415702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 AA; 42594 MW;
                                                                                                                                                                                                                                                      Query Match 24.8%;
Best Local Similarity 31.7%;
Matches 103; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A.
           NCBI_TaxID=10090;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               057466;
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RESULT 12

Anguilla

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54 IFMVNLTMADLLELYTLPLMIVYYINQGDMILPKFICNLAGCFFFINTYCSVAFLAVITY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDSGSEQ-----NGSVTSC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 WAYCTVLAVFVICEVPHHLVQ-LPWTLAELGFQDTDFHQGINDAHQVTLCLLSTNCVLDP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPNGIFSNNNSRNCIIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSISVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VEMINIAISDILFISTIPPRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 LELNLYKIAKLQTM-NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 FE--HYEKGSIPVLIIHIFLVFSFFLVFLIILFCNLVIIRTLLTQQVQMQRNAEVKRRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 TTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNP
                                                                                                                                                                            Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovidae; Caprinae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthbria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Yang W., Diehl J.R., Piumi F.;
"Partial Sequence of Caprine Platelet-Activating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
Yang W.S., Diehl J.R., Roudebush W.E.;
"Partial Sequence of Bovine Platelet-Activating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene.";
Submitted (SEP-2000) to the EMBL/GenBark/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE 342 AA; 39612 MW; 39D9379AED60FD4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 13, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 23.9%; Score 409.5; DB 6; Local Similarity 30.3%; Pred. No. 1.2e-25; es 100; Conservative 64; Mismatches 139;
      Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEL, AF302764; AAG39982.1; -.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfan; PP00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1: 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
      342
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                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
Platelet-activating factor receptor.
Capra hircus (Goat).
Eukaryota, Wetazoa; Chordata, Crania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 LCK------DRLHKALVITLALAAANACFNPLLYYFAGENFKDRL--------88ALR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 LLKVIENCPILDITALPFTICIAYFNSCMNPILYGFYGRNFRRNILRLIRGFGGGSAAR 324
                                   318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 VTCYCLIGRALLEARRVQSS-RSRGDEVLQMLAAVVLAFFLCWVPHQIFHFMFV----LA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 IW---ILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK-LQTMNYIALVVGCLLPFFTL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 IWAFAFLLSLPTALSRDVFTINHPNTTVCGTLDKHELSHVLVAIGLMKSVLGFLIPFVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 PIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tran Van Chuoi M., Dolphin C.T., Barker S., Clark A.J., Vinson G.P.;
Tran Van Chuoi M., Dolphin C.T., Barker S., Clark A.J., Vinson G.P.;
"Molecular cloning and characterization of the conva encoding the
angiotensin II recpetor of european eel Anguilla anguilla.";
Submitted (APR-198) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLGLAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SUHILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJO05132; CAB40835.1; --
InterPro; IPRO00276; GPCR_Rhodpsn.
InterPro; IPRO0003065; Ig_MRC.
FILED-Pro; IPRO00001; Zn_MTpeptdse.
PF00001; 7tm_1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 412.5; DB 13; Length 33.2%; Pred. No. 7.2e-26; Live 55; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRH0DOPSN.
PROSITE; PS00237; GPENDERLN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTENL_RECEP_F1_2; 1.
PROSITE; PS00129; IG_MHC; 1.
G-PROSITE; PS00142; ZINC_PROTEASE; 1.
G-PROLEID: OCUPLED ACCEPTOR: RECEPTOR: Transmembrane.
SEQUENCE 359 AA; 39997 WW; 053726AEA827C271 CR064;
                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin receptor.
Anguilla anguilla (European freshwater eel).
                                                                                                                                                                                                                                                                                                              359 AA
                                                                                                 313
                                                                                                                                  PRT;
                                                                                                 KD------RLKSALRKGHPQKAK
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 FB--HYEKGSIPVLTIHIFLVFSFFLVFLILFCNLVIIRTLTTQQVQIQRNAEVKRRAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 TIIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VEMINLAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDSGSEQ-----NGSVTSC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
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MEDLINE-22354683; PubMed-12466851;
MEDLINE-22354683; PubMed-12466851;
The FANTON Consortium,
the FANTON Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002)
Mature 420:563-573(2002)
BMBL; AR032547; BAC27919.1; -.
SEQUENCE 341 AA; 39175 MW; 25F97C6472797386 CRC64;
                                                                                                                              He B., Tiemann U., Kanitz W., Weikard R., Laurent P., Schwerin M., Schmidt P., "Molecular characterization of bovine platelet-actvating factor receptor transcripts and their detection in different tissues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 23.7%; Score 406.5; DB 6; Length 342; Similarity 30.3%; Pred. No. 2.1e-25; Ob. Conservative 63; Mismatches 140; Indels 27;
                                                                                                                                                                                                                                                          cattle.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AF187321; AAF01943.;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7fm_1; -.
PRINTS; PR00027; GPCRRHODPSN.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS00237; GPCRHLODPSN.
                                  Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 AA; 39691 MW; 7C4236205AE937C9 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet activating factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 LLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
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                                                                                                   SEQUENCE FROM N.A.
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SECUENCE
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174 FEHYEPYRGPILVVHVFIAF---CFFLVFFLIFYCNLVIIHTLLTQPMRQQRRAGVKRRA 230
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                                                                                                                                                                                                                                                                                                                                                                                                    172 LE-LNLYKIAKLQTMNYIALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 LITIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFN 285
                                                                                                                                                                                                                                            59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
                                                                                                                                                                                                                                                                                                                                                               119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGS------EQNGSVTSC 171
                                                                                                                                                                    1 MEHNGSFRVDS-----EFRYTLFPIVISVIFILGVVANGYVLMVFANLYPSKKLNEIK 53
                                                                                                                         1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
                                                              30;
      Length 341;
                                                                 Indels
   23.3%; Score 399; DB 11;
30.5%; Pred. No. 8.7e-25;
iive 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 PVIYCFLTKKFRKHLS --- EKFYSMRSSRKC 316
Query Match 23.3%
Best Local Similarity 30.5%
Matches 101; Conservative
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Search completed: October 8, 2003, 08:30:34 Job time : 102 secs us-09-991-225-2.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein October 8, 2003, 08:26:59; Search time 21 Seconds (without alignments) 664.885 Million cell updates/sec Run on:

0S-09-991-225-2 1712 1 MEPNGTESNNNSRNCTIENF.........KAKIKCVFPVSVWLRKETRV 330 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

328717 seqs, 42310858 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/ptoMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcdMS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	-2 Sequence 2,	.2 Sequence 2,	-2 Sequence 2,	-44 Sequence 44,	-3	4 Sequence 44,	4 Sequence 44,	Sequence 32,	4 Sequence 44,		82 Sequence 182	Sequence 374		Sequence 4,	Sequence 4,	4 Sequence 4,	4 Sequence 4,	-78 Sequence 78,	4 Sequence 4,	7 Seguence 17,	30	30 Sequence	Sequence			2 Sequence	-3
SUMMARIES	ID	US-09-585-876	-044-	US-09-586-924	US-08-153-848	812-	US-09-299-843	US-09-088-337B-4	US-09-170-496	PCT-US93-1115	PCT-US95-07180-2	US-09-170-496	US-08-513-974	US-08-559-524A-4	US-08-749-707	õ	US-08-352-678	US-09-536-954	US-09-170-496D	39	-852-	-467-	-467-	US-08-467-948	US-08-467-947	-170-	US-08-781-250-	US-09-102-710B
	DB	4	m	4	Н	7	ო	4	4	S	S	4	m	~	m	Н	m	4	4	S	m	N	m	~	3	4	m	4
	Length	346	337	337	339	339	339	339	339	339	339	339	362	373	373	361	361	361	361	361	348	302	302	344	344	361	370	374
о*	Query Match	99.5	32.7	32.7	28.0	28.0	28.0	28.0	28.0	28.0	28.0	27.8	26.9	25.8	25.8	25.7	25.7	25.7	25.7	25.7	25.7	25.6	25,6	25.5	25.5	25.4	25.1	24.5
	Score	1703	559	559	479	479	479	479	479	479	479	476	461	442	442	440	440	440	440	440	439.5	3	m	437	437	434	4.30	419.5
	Result No.	1	2	m	4	5	ø	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346

Sequence 373, App Sequence 9, Appli Sequence 2, Appli	inni	ຕັຕັ	Sequence 6, Appli Sequence 6, Appli	Sequence 6, Appli Sequence 6, Appli	Sequence 6, Appli Sequence 6, Appli	53,	24,	4
US-08-513-974B-373 US-08-988-876-9 US-08-442-134A-2	US-08-444-581B-2 US-08-446-088A-2	US-08-749-707-3	US-08-097-938-6 US-08-476-000-6	US-08-472-840-6 US-08-476-976-6	US-08-474-410-6 US-08-486-673B-6	US-09-045-583-53 US-09-534-185-53	US-08-405-271A-24 US-08-097-938-4	US-08-476-000-4
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373	375	375	308 308 808	398 398	398 398	355	347	398
24.3	24.3	24.3	23.7	23.7	23.7	23.7	23.4	23.4
416.5 416 416	4 4 4 4 16 4 16 6 16 6 16 6 16 6 16 6 1	416	406.5	406.5	406.5	405	401	400.5
2008	32	33	32 36	37	39	41	43	45

ALIGNMENTS

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121 FLAMVHPPRILHUTSIRSAMILCGIIMILIMASSIMILDSGSEONGSVTSCLEENLYXIA 180 [[[[[[[]]]]]]][[[[[]]]]]]] 137 FLAMVHPPRILHUTSIRSAMILCGIIMILIMASSIMILDSGSEONGSVTSCLEINLYKIA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MINIAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 MEDNGTESNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSISVNVF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                Sequence 2, Application US/09585876

Patent No. 6586205

GENERAL INFORMATION

APPLICANT: Glucksmann, Maria Alexandra

APPLICANT: Glucksmann, Maria Alexandra

APPLICANT: Silos-Santiago, Immaculada

TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and

TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and

TITLE OF INVENTION: USes Thereof

FILE REFERENCE: 8600-88

CURRENT FALING DATE: 2000-06-01

EARLIER APPLICATION NUMBER: 60/182,061

EARLIER FILING DATE: 2000-06-01

SARLIER FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 2

SOFFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.5%; Score 1703; DB 4; Best Local Similarity 99.4%; Pred. No. 2.1e-124; Matches 328; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-585-876-2
RESULT 1
US-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: 1
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248 PYHIQRIIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 RILHVTSIRSAWILCGIIWI-LIMASSIMLIDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 337;
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CDNA CLONE HWIMER! THAT ENCODES A NOVEL ITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR FILE REFERENCE: GH-70001-1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 559; DB 4;
Pred. No. 4.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/844,795
PRIOR FILLING DATE: 1997-04-22
NUMBER OF EDGLID NOS: 2
SOFTWARE: FRREISEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/586,924 CURRENT FILING DATE: 2000-06-05 PRIOR APPLICATION NUMBER: 09/044,404
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Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                        Sequence 2, Application US/09586924 Patent No. 6506878
                                                                                                                                                                                                                            SATHE, GANESH M.
HALLSEY, WENDY
ELLIS, CATHERINE E.
AMES, ROBERT S.
FOLLEY, JAMES J.
SARAU, HENRY M.
CHAMBERS, JON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.0°
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HOMO SAPIENS
US-09-586-924-2
                                      302 SALRK 306
                                                                          307 STFRK 311
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                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SATHE, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER
SOFTWARE: FASE
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-153-848-44
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 NSRNC--TIENFKREFFPIVYLLIFFWGYLGNGLSIYVFLQPYKKSTSYNVFMLNLAISD 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                           APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: EMES', CATHERINE
APPLICANT: FOLEY, JAMES
APPLICANT: FOLEY, JAMES
APPLICANT: SARAY, HENRY
APPLICANT: SARAY, HENRY
ITLE OF INVENTION: CDNA CLONE HATMEBI THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.7%; Score 559; DB 3; L6 38.0%; Pred. No. 4.5e-36; Live 71; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: DS/09/044,404A.
FILING DATE: MARCH 19, 1998
                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation
STREET: 790 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34,344
ER: GH-70001-1
                                                    Sequence 2, Application US/09044404A Patent No. 6200775
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  STALL.
COUNTRY: USA
ZIP: 19406
ZNPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"TOTAL TIBM COMPATIBLE
TOTAL
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFHONE: 610-270-5219
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.7%
Best Local Similarity 38.0%
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-044-4048-2
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                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-044-404A-2
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APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                              SOFTWARE: DOS SUFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATHRON DATE:
                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PE-0237 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J
REJISTRATION NUMBER: 36,749
REFERENCE/DOCKET WINBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 amino acids
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Best Local Similarity 34.89
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
CLONE: 992700
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                                                                                                                                                              Palo Alto
                                                                                                                                                                                                     USA
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US-09-299-843A-44
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                                                                                                                                                                               STATE: C. COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 HPVKSLKLRRPLYAHLACAFLWVVAVAWAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 LCFLPYHTLRTVHLTTWKV~-GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FSNNNSRNCIIEN-PKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 FSLATAEQCGGETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Gaps
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%; Score 479; DB 1; Length 33(34.8%; Pred. No. 6.8e-30;
tive 62; Mismatches 126; Indels
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                               STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977/452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,3022
REGISTRATION NUMBER: 35,3022
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 3, Application US/08812871
; Patent No. 595303
; Patent No. APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 3179.
RELEPRA: (312) 474-6300
TELEPRA: (312) 474-6448
TELER: 25-3866
INFORMATION FOR EMPLY SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
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Best Local Similarity 34.8
Matches 112; Conservative
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; MOLECULE TYPE: protein
US-08-153-848-44
                       NUMBER OF SEQUENCES:
                                                                                                                                                                 USA
                                                                                                                                                            COUNTRY:
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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125 185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241 246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLISLNGALDPIMYFFVAEKFR 305 HPFRILHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184 242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297 7 FSNNNSRNCTIEN-FKREFFFIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65 22; Gaps 28.0%; Score 479; DB 2; Length 339; 34.8%; Pred. No. 6.8e-30; Live 62; Mismatches 126; Indels

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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               =
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Gray, Patrick W.
Schweikart, Vicki L.
TILLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 479; DB 4; Length 339; Pred. No. 6.8e-30; 62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               =
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APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CIASSIFICATION: CURNOWN
PRIOR APPLICATION DATA:
APPLICATION MUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6346874 and, Greeta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLEGULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44
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                                                                                  306 HALCULLCGKRLKGPPPSFEGK 327
                                                                                                                                                                                                                                                                                      Sequence 44, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
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34.8%;
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STATE: Illinois
COUNTRY: USA
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Best Local Similarity 34.89
Matches 112; Conservative
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                                                                                                                                                                                                                  RESULT 7
US-09-088-337B-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYFFAGENFK 297
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                                                                       GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Partick W.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweisert, Vicki L.
APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD. APPLICANT: CARD.
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                                                                                                                                                                                                                                                                                                                                                                                            6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
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REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
FELECOMMUTCATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6448
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RIOR APPLICATION DAMBER: US 09/088,337
FILING DATE: 01-0UN-1998
RIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
RIDING DATE: 17-NOV-1992
ATTORIEY/AGENT INFORMATION:
Sequence 44, Application US/09299843A
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SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.8<sup>th</sup>
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 CITY: Chicago STATE: Illinois
                                         Patent No. 6107475
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192 HALVSIAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
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75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFEFYLNMYASIYFLTCISADRFLAIV
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APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
       Tower, 233 South Wacker Drive
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/11153
                                                                                                                                                                                                                                                                                                                                                US 07/977,452
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                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   35,302
RR: 31794
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31
TELECONMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 amino acids
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                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein PCT-US93-11153-44
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    6300 Sears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
                                                      Illinois
                            Chicago
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                                                                           COUNTRY:
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TILE OF INVENTION:
FIRE REPERENCE: AREN-0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPVKSLKLRRPLYAHLACAFLWVVAVAWAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
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192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
                                                                                246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPINYFFVAEKFR 305
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                                                 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
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Sequence 44, Application PC/TUS9311153
SEQUENCAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                      298 DRLKSAL----RKGHPQKAKTK 315
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34.8%;
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Best Local Similarity 34.8
Matches 112; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 RESULT 8
US-09-170-496D-32
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PCT-US93-11153-44
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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
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Parcert No. 6114139

GENERAL INFORMATION

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Masaki

APPLICANT: Fujii, Ryo

APPLICANT: Pujii, Ryo

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Ohtaki, Shoji

APPLICANT: Ohtaki, Razuhiro

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

TITLE OF INVENTION: G PROJECTION, AND USE THEREOF
                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                ;; Score 476; DB 4; Length 336;; Pred. No. 1.2e-29;
61; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
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FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 DRLKSAL ----RKGHPQKAKTK 315
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MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SISTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn version 3.1 SEQ ID NO 182 LENGTH: 339
                                                                                                                                                                                                                                       27.8%;
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 34.89
Matches 112; Conservative
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                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-170-496D-182
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US-08-513-974B-374
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NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
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                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION PATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DAPE: 06-UONE-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCORDITION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 32580
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
ADDRESSE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUNE-1995
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                                                                                                                                                                                                       COMPUTER READABLE FORM:
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US-09-170-496D-182
                                                                                                                                 COUNTRY: UR
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373 amino acids
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; MOLECULE TYPE: protein
US-08-559-524A-4
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                                                                                                                                                                                                             STATE: D.C. COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 IITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Mismatches 114; Indels
                                                                                                       PALICATION NUMBER: UP 6-32611

PRILING DATE: 28-DEC-1994

PRICATION WIMBER: UP 6-32611

PRILING DATE: 28-DEC-1994

PRICATION NUMBER: UP 6-270017

PILING DATE: 02-NOV-1994

PRICATION NUMBER: UP 6-236357

PILING DATE: 30-SEP-1994

PRICATION NUMBER: UP 6-236356

PILING DATE: 30-SEP-1994

PRICATION NUMBER: UP 6-236356

PILING DATE: 30-SEP-1994

PRICATION NUMBER: UP 6-189274

                                                FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION ATA:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 6-189273
FILING DATE: 11.AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11.AUG-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
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312 LYFLAGDTFRRLSRATRK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEC 1D NO: 374: SEQUENCE CHARACTERISTICS: LENGTH: 362 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 45:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Resnick, David S. REGISTRATION NUMBER: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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Matches 98; Conserv
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US-08-559-524A-4
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45 TKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----LNLYKIAKLQTMN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 KKNAVTISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT-- 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TIENFKREFFPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 YIALWVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.8%; Score 442; DB 2; Length 37 Best Local Similarity 31.0%; Pred. No. 5.4e-27; Matches 95; Conservative 78; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15.NOV-1995
Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Oolley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   044481-5010-00-US
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN, LEWIS & BOCKIUS LL.P
STREET: 1800 M Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGIET, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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192 SLPWILLGACFIGYVLPLIILLCYSQICCKLFRTAKQNPLTEKSGV---NKKALNTILL 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NLAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSI-MLLDSGSEQNGSVTSCLEL-NLYKIA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 PSATPOGNDCDLYAHHSTARIVMPLHYSLVFIIGLVGNLLALVVIVQNRKKINSTTLYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%; Score 440; DB 1; Length 361; 32.1%; Pred. No. 7.4e-27; tive 63; Mismatches 135; Indels
MUNESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., STREET: Suite 600 CITY: Washington STATE: D.C. COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 YYFAGENFKDRLKSALRK 306
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                                                                                                                                                                                                                                                                                                                                            COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acids
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Best Local Similarity 32.13
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IRSAWILCGIIWILIMASSIMLL----DSGSEQNGSVTSCLE-----LNLYKIAKLQTMN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 YHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 TIENFKREFFPIVYLIIFFWGYLGNGLSİYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Riseff, Mark
APPLICANT: Riseff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOKERR: US/08/749,707
FLING DATE: 15-NOV-1996
CLASSIFICATION: 536
                                                       APPLICANT: Jantzen, Hans-Michael
IITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Adler, Reid G.
REGISSRATION NUMBER: 30,988
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
                                                                                                                                                                                                         E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               APPLICANT: Conley, Pamela B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.0%
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20036-5869
COMPUTER READABLE FORM:
                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, L
                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 KSALRK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-383-750-4
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8, 2003, 08:27:32; Search time 30 Seconds (without alignments) 1772.413 Million cell updates/sec
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/cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                600653 seqs, 161128416 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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110.
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                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                            Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 14, Appli Sequence 14, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
SUMMARIES	US-09-826-791-2 US-09-991-25-2 US-09-991-25-55 US-09-826-791-6 US-09-866-230-7 US-09-866-230-9 US-09-728-478-2 US-09-728-478-2 US-09-729-679-26 US-10-779-679-26 US-10-321-807-14 US-10-321-807-14 US-10-321-807-889 US-10-231-807-88
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Result	1111111 128790087901

Sequence 8, Appli Sequence 5, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1, Appli		equence 14 guence 12, quence 2, equence 4, equence 8, equence 8,	Sequence 12, Appl. Sequence 14, Appl. Sequence 14, Appl. Sequence 32, Appl. Sequence 6, Appli. Sequence 6, Appli. Sequence 104, Appli.
US-09-866-23 US-09-828-47 US-09-779-67 US-09-91-22 US-10-25-56 US-10-167-19 US-09-94-798 US-09-948-798	US-10-017-161-5 US-10-278-141-2 US-10-10-568-2 US-10-321-807-5 US-10-023-775B- US-10-270-144-2 US-10-270-144-2 US-10-188-465-8	US-10/0/5/384 US-10/0/25-56/1 US-09-848-889-1 US-09-788-133- US-09-928-478 US-09-991-225 US-10-349-021	US-10-100-982-1 US-10-268-332-1 US-09-964-8118-1 US-10-251-385-3 US-09-828-478-6 US-10-349-021-6 US-10-225-567A-
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ALIGNMENTS

61 MINLAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120 09 09 1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF Gaps .; 0 Length 330; Indels TITLE OF INVENTION: No. US20010039037Alel Polypeptide
FILE REFERENCE: PC10914ADAM
CURRENY APPLICATION NUMBER: US/09/826,791
CURRENY FPLICATION NUMBER: 00/09/826,791
FRIOR PILLING DATE: 2001-04-05
PRIOR FILLING DATE: 2000-04-05
PRIOR FILLING DATE: 2000-04-05
PRIOR RELING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 330 100.0%; Score 1712; DB 9; 100.0%; Pred. No. 1.1e-140; tive 0; Mismatches 0; ; Sequence 2, Application US/09826791; Patent No. US20010039037A1; GENERAL INFORMATION: Best Local Similarity 100.0 Matches 330; Conservative ORGANISM: Homo sapiens RESULT 1 US-09-826-791-2 ; ORGANISM: HC US-09-826-791-2 TYPE: PRT Query Match g ŏ δŽ QQ δŽ

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APPLICANT: Pfizer Inc
TITLE OF INVENTION:
FILE REFERENCE: PC10914aDAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19
NUMBER OF SCO ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1712; DB 12;
100.0%; Pred. No. 1.1e-140;
tive 0; Mismatches 0; 1
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100.0%; Pred. No. 1.2e-140;
tive 0; Mismatches 0;
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Patent No. US20010039037A1
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 330; Conservative
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Matches 330; Conservative
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US-09-826-791-6
                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-991-225-55
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US-09-826-791-6
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TITLE OF INVENTION: A NOVEL HURAN G-PROTEIN COUPLED RECEPTOR, HGPRBWY11, EXPRESSED HI
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REPRERENCE: D0075.NP
CURRENT FILING DATE: 2001-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
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PRIOR FILING DATE: 2000-10-17
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                                                                                                       241 FLCELPYHTLRTVHLITWKVGLCKDRLHKALVITLALAAANACFNPLLYTFAGENFKDRL 300
           181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
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; Pred. No. 1.1e-140;
0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09991225 Publication No. US20030153063A1 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 330; Conservative
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APPLICANT: Murphy, Andrew, et al.
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: NO. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of
FILE REPRENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60,207,725
PRIOR APPLICATION NUMBER: 60,207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Proctain
TITLE OF INVENTION: Proctain
TITLE OF INVENTION: Proctain
TITLE OF THE REFERENCE: 04974.00458
CURRENT APPLICATION NUMBER: 05/09/828,478
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR PILING DATE: 2000-12-13
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                    US-09-866-230-9; Sequence 9, Application US/09866230; Sequence 9. Application US/09866230; Patent No. US20020150901a1; CENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 330; Conservative
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US-09-866-230-9
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LENGTH: 346
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US-09-828-478-2
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TITLE OF INVENTION: No. US20020150901Alel Nucleic Acids, Polypeptides, Methods of Mak
FILE OF INVENTION: No. US20020150901Alel Nucleic Acids, Polypeptides, Methods of Mak
FILE OF REPERENCE: REG 771A
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEO ID NOS: 9
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                   MEDNGTESNNNSRNCTIENEKREFFPLYYLLIFFWGYLGNGLSIYVFLQPYKKSISVNVF 76
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APPLICANT: Yerlack, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Mimberly A
APPLICANT: Andrew, David P
APPLICANT: Andrew, David P
APPLICANT: Meses, Peter S
TILLE OF INVENTION: No. US20030082757Alel Proteins and Nucleic Acids Encoding the
FILE REPERENCE: 12566-661
CURRENT FILING DATE: 2001-02-08
FRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR APPLICATION NUMBER: USSN 60/18191
PRIOR APPLICATION NUMBER: USSN 60/18191
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
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Pred. No. 1.2e-140;
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APPLICATION NUMBER: USSN 60/219585
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Publication No. US20030082757A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond J
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchernev, Velizar T
APPLICANT: Tchernev, Valizar T
APPLICANT: APPLICANT: Casman, Stacie
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Vernet, Corine A
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SEQ ID NO 2
LENGTH: 346
TYPE: PRI
ORGANISM: Homo sapiens
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Best Local Similarity
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CURRENT APPLICATION NUMBER: USSN 60/181045
PRIOR PLING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/18099
PRIOR PLING DATE: 2000-02-17
PRIOR PLING DATE: 2000-02-09
PRIOR PLING DATE: 2000-02-09
PRIOR PLING DATE: 2000-02-09
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PRIOR PRILING DATE: 2000-02-09
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                              Length 346;
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                              DB 10;
                         Query Match 100.0%; Score 1712; DB 10; Best Local Similarity 100.0%; Pred. No. 1.2e-140; Matches 330; Conservative 0; Mismatches 0;
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APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchernev, Vellzar T
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Casman, Stacie
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SOFTWARE: Patentin Ver. 2.0
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     61 MINLAISDILFISTIPFRADYTIRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR
                      1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
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                                                                                                                                              KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF
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Sequence 2, Application US/10349021

Publication No. US20030157541a1

GENERAL INFORMATION:

TITLE OF INVENTION: Regulation of Human Cyslf2-Like GPCR

TITLE OF INVENTION: Protein

FILLE OF INVENTION PROTEINS US/09/828,478

PRIOR FILLING DATE: 2001-04-09

PRIOR FILLING DATE: 2001-04-07

PRIOR FILLING DATE: 2000-04-07

PRIOR FILLING DATE: 2000-04-07

PRIOR FILLING DATE: 2000-12-13

NUMBER: OF SEQ ID NOS: 16

SOFTWARE: FRASESQ for Windows Version 4.0
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100.0%; Pred. No. 1.2e-140;
1ive 0; Mismatches 0;
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Sequence 30, Application US/09991225

Sequence 30, Application No. US20030153063A1

GENERAL INFORMATION:

SETTIATE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

HEART AND VARIANTS THEREOF
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Pred. No. 1.2e-140;
Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/991,225
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                  0; Mismatches
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
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1 Similarity 100.0%; P
330; Conservative 0;
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                                                   NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                  Conservative
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US-09-991-225-30
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US-09-779-679-26
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                                                                                       SEQ ID NO 26
LENGIH: 346
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Best Local S
Matches 330
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Best Local S:
Matches 330,
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y aPPLICANT: Chen, Rupong
APPLICANT: Chen, Rupong
APPLICANT: Lowitz, Revinb
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION NUMBER: US/09/714,008
PRIOR PILING DATE: 1999-11-17
PRIOR PILING DATE: 1999-11-17
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,088
PRIOR PILING DATE: 1999-11-17
     Sequence 589, Application US/10225567A

Sequence 589, Application US/10225567A

Publication No.

September Interpretation:

APPLICANT: LiteSpan Blosciences

APPLICANT: Burner. Glenna C.

APPLICANT: Burner. Glenna C.

APPLICANT: Burner. Glenna C.

APPLICANT: Runsh. Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEP

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR PELICATION NUMBER: 5000-12-19

NUMBER OF SEQ ID NOS: 2292

SEQ ID NO 589

LENGTH: 346
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ilarity 100.0%; Pred. No. 1.2e-140;
Conservative 0; Mismatches 0;
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Publication No. US20030166148A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity
US-10-225-567A-589
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US-10-225-567A-589
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Matches
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APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
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PRIOR APPLICATION NUMBER: 60/181,749
PRIOR FILING DATE: 2000-02-11
Remaining Prior Application data removed - See File Wrapper or Palm. NUMBER OF SEQ ID NOS: 133
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                                                                                                                                                                                                                                                      TILE OF INVESTION RECEDENCES
CURRENT APPLICATION NUMBER: US/10/321,807
CURRENT RILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/9/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 1999-11-17
PRIOR PLILING DATE: 1999-11-17
PRIOR PLILING DATE: 1909-11-17
PRIOR PLILING DATE: 1909-11-17
PRIOR PLILING DATE: 1909-11-17
PRIOR PLILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-11-17
                                                                   Sequence 14, Application US/10321807
Publication No. US20030166148A1
GENERAL INFORMATION:
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                         RESULT 12
US-10-321-807-14
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completed: October te : 32 secs
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692 or 58874

FILE REFERENCE: MPI2001-288P1(M)
CURRENT APPLICATION NUMBER: US/10/290,078

CURRENT FILING DATE: 2002-11-07

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/166,099
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,369
PRIOR APPLICATION NUMBER: 60/171,902
PRIOR APPLICATION NUMBER: 60/171,902
PRIOR PILING DATE: 1999-12-23
PRIOR PLING DATE: 1999-12-23
PRIOR PRIOR DATE: 1999-12-23
PRIOR PRIOR DATE: 1999-12-23
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 133
SEQ ID NO 88
SEQ ID NO 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
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                                                                                                                                                                                                                                                                                                                                                                                  Score 1706; DB 12; Length 346;
Pred. No. 3.8e-140;
0; Mismatches 1; Indels 0
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Publication No. US20030124596A1
GENERAL INFORMATION:
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Matches 329; Conservative
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US-10-321-807-88
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ORGANISM: Homo Sapien
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US-10-290-078-21
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LENGIH: 337
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                                                                                                                                                                                                                                                                                                                                      246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
  68
11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
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4: /SIDS1/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*
5: /SIDS1/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*
7: /SIDS1/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*
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1712
1 MEPNGTESNNNSRNCTIENF.......KAKTKCVFPVSVWLKKETRV 330
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human G-protein co	Human G-protein co	Human G-protein co	Human G-protein co	Human G-protein co	Human P2Y-like GPC	Human G-protein co	Human G-protein co	Cysteiny] leukotri
SUMMARIES	, QI	AAG77964	ABU11900	AAE07539	ABU11939	AAE12022	AAB82852	AAE07538	AAU04368	AAU07294
	DB	23	24	22	24	22	22	22	22	22
	Query Match Length DB	330	330	341	341	346	346	346	346	346
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	1712	1712	1712	1712	1712	1712	1712	1712	1712
	Result No.	П	7	æ	4	ហ	Q	7	80	ov

Human LTC4 recepto	Human GPCR polypep	Human novel polype	Human CysLT2-like	Human CysLT2 GPCR	Human G-protein co		Human cysteinyl le	Human G-protein co	Human G-protein co	Human G-protein co	Truncated cysLT2 c	Human cysLT2 cyste	Human HGPRBMY11 N-	n HGPRBM	Pig LTC4 receptor	CYSL	Rat LTC4 receptor	Human protein sequ	A human 7-transmem	Human 7-transmembr	Human cysLT-like r		Human cysteinyl le	Human cysteinyl le	Human G protein co	Human G-protein co	Human GPCR polypep	Human Purinoceptor	Human G-protein co	Human novel polype	Human G protein-co	Human G-protein co	Human P2Y-like rec	R89	٠ بر
\sim	ABP95624	IO	AAU10004	723	96	22	ABP81707	92	38	AAE08553		50	ABU11962	ABU11963	AAB73098	AAB85095	AAB73099	AAM25841	AAW85047	AAW75799	AAB85096		ABP81686	ABU11904	S	AAU04375	ABP95602	\simeq	38	ABG70287	AA015399	ABB81902	88	2180	ABB79438
22	23	23	23	23	23	23	24	24	22	22	22	22	24	24	22	22	22	22	19	13	22	22	24	24	77	22	23	23	23	23	33	23	23	23	23
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10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAG77964 standard; Protein; 330 AA.

RESULT 1 AAG77964 AAG77964;

Human, G-protein coupled receptor; GPCR; PFI-017; cytostatic; neoplastic; antiallergic; osteopathic; cardiovascular; immunosuppressive; gene therapy; heart disease; gastrointestinal disease; sleep disorder; immunological disorder; bulmonary disorder; infectious disease; myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity; chronic obstructive pulmonary disease; inflammatory bowel disease; inflammatory bowel disease; inflammatory concer; osteoporosis; cardiovascular disease; inflammation, cancer; osteoporosis; cardiovascular disease; infection; allergy; respiratory disease; sensory organ disorder; hair loss; immunological disorder; pulmonary disease; neoplastic disease; vasculitic granulomatous disease; dermatology; psychotherapeutic. Human G-protein coupled receptor PFI-017 (first entry) US2001039037-A1 Homo sapiens 25-FEB-2002 08-NOV-2001

05-APR-2001; 2001US-0826791.

05-APR-2000; 2000GB-0008504. 19-APR-2000; 2000US-198367P.

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The sequence represents a novel G-protein coupled receptor (GPCR), PPT-017 of the invention. The PPI-017 has cytostatic, antialistic, cardiovascular, and immunosuppressive activity. The corepathic, cardiovascular, and immunosuppressive activity. The polynucleotides may have a use in gene therapy. The polynucleotide is useful for treating allergic disorders, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder is manual personal disorder is an allergic chinitis or a sthma, the pulmonary clisease. PPT-017 polynucleotide sequences may be used for the diagnosis of disease. PPT-017 polynucleotide sequences may be used for the diagnosis of diseases resulting from expression of PPT-017, and to detect and quantify of per expression in conditions, disorders or diseases in which can mapped in conditions, disorders or diseases in which can modilate the peptide can be used to produce anti-PPI-017 activity may be implicated. The polypeptides are used to produce anti-PPI-017 activity may be implicated. The polypeptides are used to produce compositions which can modilate the peptide can be used in treating compositions which can modilate the peptide can be used in treating observed infections, allergy and respiratory disease, of disease, inflammation, cancer, osteoporosis, cardiovascular disease, sensory organ discorders, allergy and respiratory disease, and heart diseases, produced and psychotherapeutics.
                                                                                                                                                                                           useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
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                                                                                                                                                                                 New PFI-017 protein and polynucleotide encoding the protein, un diagnosing or treating metabolic diseases, urogenital disease, immunological disorders, infectious diseases, neoplastic or myeloproliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1712; DB 23; Length 330; 100.0%; Pred. No. 5.4e-177; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                            Claim 7; Fig 6B; 39pp; English.
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Matches 330; Conservative
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                       (HARL/) HARLAND L.
                                                                                                                                          N-PSDB; AAH77276.
                                                                       Harland L;
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                                                       FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA
                                                                                                                                            241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
                                                                                                                              181 KLQTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLIF
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ABU11900 standard; Protein; 330 AA.
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RESULT 2

Sequence

The invention relates to an isolated polypeptide (designated HGPRBMIII), which has a G-protein coupled receptor (GPCR) activity (also known as GPCRAL) and ise encoded by the DDNA contained in ATCC Deposit Number PrA-2766, its variants (JGPRBMYIIV1 and RGPRBMYIIV2), fragments, domains, species homologues and proteins 95% similar to it. Also included are: (1) the mucleic acids); (2) recombinant vectors; (3) transformed host eclas expressing HGPRBMYII); (4) an anti-HGPRBMYII proteins (including variants, fragments, complements and sequences 95% similar to the HGPRBMYII nucleic acids); (2) recombinant vectors; (3) transformed host condition in a subject; (6) identifying a binding partner to the HGPRBMYII polypeptide; (7) identifying a binding partner to the condition in a subject; (6) identifying a binding partner to the HGPRBMYII polypeptide; (7) identifying a binding partner to the condition of (8); and (10) screening for candidate compounds capable of having altered GPCR activity; (9) a shuffled polymucleotide produced by the mathod of (8); and (10) screening for candidate compounds capable of binding to and/or modulating activity of a GPCR. The polypeptide or the polymorleotide is useful for preventing, treating or ameliorating a medical condition, particularly cardiovascular diseases of disorders, cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBMYII polypeptide or polynucleotide is also useful for treating or preventing or ameliorating each of medical conditions, syndrome (ADES), leukamia, sepsis, and munnodeficiency virus (HTV) infections, schizophrenia, sleeplessness, acquired immunodeficiency virus (HTV) infections, schizophrenia, sepsiles (mannodeficiency virus (HTV) infections, schizophrenia, sepsiles (mannodeficiency virus (HTV) infections, schizophrenia, sepsiles (mannodeficiency virus (HTV) infections, schizophrenia, sepsiles).

The present sequence represents an HGPRBMYII protein (or variant). Human, receptor; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR61; GPcrotein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obseity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; ALDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia; polynucleotide, useful for preventing, treating or ameliorating e.g. myocardial infarction, angina, thrombosis, Alzheimer's disease, schizophrenia, AIDS, lenkemia New human G-protein coupled receptor HGPRBMY11 polypeptide or Barber LE; Cacace AM, Human G-protein coupled receptor HGPRBMY11. Ramanathan C, Claim 11; Fig 1; 444pp; English. (BRIM) BRISTOL-MYERS SQUIBB CO 17-NOV-2000; 2000US-249613P. 21-DEC-2000; 2000US-257611P. 16-JUL-2001; 2001US-305818P. 16-NOV-2001; 2001WO-US44019 (first entry) Nelson TC, WPI; 2003-093137/08 N-PSDB; ABX56007 WO200286123-A2. Homo sapiens. 13-FEB-2003 31-0CT-2002. Feder J,

us-09-991-225-2.rag

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                                                                                                    MENLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFITVLSVVR 120
                                                                                                                                                   FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                                                                                                     KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
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                                                                                                                 1 MEPNGTESNNNSRNCTIENFKREFFPIVYLIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; hypertension; congenital heart defect; anorexia; atrial septal defect; ventricular septal defect; valve disease; scleroderma; obesity; transplantation; adrenolewcodystrophy; AIDS; congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer; haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia; acquired immune deficiency syndrome; disbetes; infectious disease; metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD; neurodegemerative disorder; Alzheimer's disease; immune disorder; fertility; parkinson's disorder; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; GPCRX; GPCR1b; cardiomyopathy;
                           0
  DB 24; Length 330;
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human G-protein coupled receptor 1b (GPCR1b) variant.
                                                                                                                                                                                                                                                                                                                       KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                          Mismatches
100,0%; Score 1712;
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide
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2000US-0183191.
2000US-0219585.
             100.08;
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2000US-0181157.
2000US-0181339.
2000US-0181344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                          Conservative
             Similarity
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17-FEB-2000;
20-JUL-2000;
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09-FEB-2000;
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           Best Local Sim
Matches 330;
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Query Match
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GPCRX sequences are used to treat or prevent a human suffering trom GPCRX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosis, pulmonary stenosis, subacortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, sclerodama, obseity, transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, certility, heamophilia, hypercoaquiation, idiopethic thrombocytopenic purpura, graft versus host disease, acquired immune deficiency syndrome (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and treatment of Albright Hereditary Osteodystrophy, GPCRX antibodies are used to treat a pathological state and treat or prevent disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MINLAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human G-protein coupled receptor proteins 1-7 (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, infectious disease, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disorder, immune disorders, haematopoletic disorders and various dyslipidaemias. OPCRX DNA is also useful in gene therapy. The present sequence is human GPCRIb protein variant. The GPCRI DNA is located on
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                                                                                                                                                                                                                                                              treating or preventing, e.g., cardiomyopathy, atherosclerosis, hypertension, acquired immune deficiency syndrome, bronchial asthma, Crohn's disease, and multiple sclerosis
                                                                                                                                                                                                                                              Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for
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                                                                                                                         Andrew
                                                                                                        Mishra VS;
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Li L, Spytek KA,
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                                                                                                    Padigaru M,
Vernet CAM,
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20-JUL-2000; 2000US-0219758.
26-JUL-2000; 2000US-0221341.
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Ballinger R,
                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                   WPI; 2001-497077/54.
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Best Local Similarity
Matches 330; Conserv
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                                                                                                      Taupier RJ,
                                                                                                                           Casman S,
                                                                                                                                           Mezes PS;
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which has a G-protein coupled receptor (GPCR) activity (also known
as GPCR4 or GPCR31) and is encoded by the CDNA contained in ATCC Deposit
Number PTA-2766, its variants (IGPRBWI11) and HGPRBWI119), fragments,
domains, species homologues and proteins 95% similar to it. Also included
care: (1) the nucleic acids); (2) recombinant vectors; (3) transformed host
calls expressing HGPRBWI11; (4) an anti-HGPRBWI1 intibody; (5)
HGPRBWI11 nucleic acids); (2) recombinant vectors; (3) transformed host
calls expressing a pathological condition or a susceptibility to a pathological
condition in a subject; (6) identifying a binding partner to the
HGPRBWI11 polypeptide; (7) identifying an activity in a biological assay;
(8) a process for making polynuclectide sequences encoding a gene product
having altered GPCR activity; (9) a shuffled polynuclectide produced by
the method of (8); and (10) screening for candidate compounds capable of
binding to and/or modulating activity of a GPCR. The polypeptide or the
polynuclectide is useful for preventing, treating or ameliorating a
medical condition, particularly cardiovascular failure, aribythmias,
cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
thrombosis or hypertension). The HGPRBWI11 polypeptide or polynuclectide
is also useful for treating or ameliorating or ameliorating estation or all and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and acide or parking and 
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                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; cardiovascular disease; arrhythmis, amycarddal infarction; congestive heart failure; cardiomyopathy; atherosalerosis; arteriosalerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; parkinson's disease; osteoporosis; bestyt; human immunodeficiency virus infection; HTV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; HTDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischeemia;
                                                                                                                                                                                                                                                                                                                      HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
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                                                                          ABU11939 standard; Protein; 341 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000; 2000US-249613P.
21-DEC-2000; 2000US-257611P.
16-JUL-2001; 2001US-305818P.
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                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                         receptor;
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                                                                                                                                        ABU11939;
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                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, G-protein coupled receptor; GCREC; gene therapy; proteosome analysis; cell proliferative disorder; arteriosclerosis; cancer; neurological disorder; Huntington's disease; Parkinson's disease; cardiovascular disorder; Huntington's congestive heart failure; gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
                                                                                                                                                                                                                                                                                                          61 MINIAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                 121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITTLIF 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KLQIMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTIIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
                                                                                                                                                                                                        1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
                                                                                                                                                       Gaps
The present sequence represents an HGPRBMIll protein (or variant).
                                                                                                                                                     0;
                                                                                                    Length 341;
                                                                                                                                                       Indels
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                                                                                                    DB 24;
                                                                                                    100.0%; Score 1712; DB 24; 100.0%; Pred. No. 5.7e-177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human G-protein coupled receptor, GCREC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l..55
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE12022 standard; Protein; 346 AA.
                                                                                                                                                     0;
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06-APR-2000; 2000US-195155P.
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                                                                                                                                                     Conservative
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                                                                                                                            Similarity
                                                   341 AA;
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                                                                                                                                                     330;
                                                      Sednence
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                                                                                                    Query Match
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AAB82852 standard; Protein; 346 AA.
                                        AAB82852;
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                                                                                                                                                                                                                                               Key
   AAB82852
                 The present sequence is a human G-protein coupled receptor, GCREC-1
protein. The GCRECs are used for treating or preventing disorders
associated with decreased expression of functional GCREC, and for
identifying specific agonists and antagonists, also binding agents
and modulators. They can also be used for generating specific antibodies
and for protessome nallysis. Disorders that can be treated include
cell proliferative disorders, e.g., arteriosolerosis and cancer,
neurological disorders, e.g., Huntington's disease and Parkinson's
disease, cardiovascular disorders, e.g., acquired immunodeficiency
syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
cobesity and viral infections. Nucleic acids that encode GCREC are
used for identifying agents that alter its expression, for assessing
toxicity of test compounds, and as sources of primers and probes for
clamoscent mapping, and for recombinant production of GCREC. The
antibodies are useful for diagnosis and monitoring of diseases
and as therapeutic agents and for drug screening.
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                                                                             Khan FA;
                                                                            . Tang YT, Baughn MR, Graul R, Khan Fl
Lal P, Au-Young J, Yang J, Hafalia A;
                                                                                                                                                               New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 1712; DB 22; Length 346; Local Similarity 100.0%; Pred. No. 5.8e-177; Local Similarity 0.9 Mismatches 0; Indels 0;
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                                                                                                                                                                                                                   111pp; English
           28-APR-2000; 2000US-200551P.
05-MAY-2000; 2000US-202278P.
 2000US-199084P.
                                                   (INCY-) INCYTE GENOMICS INC.
                                                                           CM,
                                                                                        Patterson C,
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                                                                                                                                                                                                                   Claim 1; Page 101-102;
                                                                                                                          WPI; 2001-616472/71.
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                                                                                                                                      N-PSDB; AAD19577
20-APR-2000;
                                                                           Policky JL,
                                                                                        Nguyen DB,
                                                                                                   Walia NK,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a P2Y-like G-protein coupled recepto (GPCR) that has 7 transmembrane regions. Homology searches showed this receptor to be homologous to cysteinyl leukotriene (cycLTI LTD4) receptor and P2X receptors. The invention provides P2Y-like GPCR polypeptides and polynocleotides, expression vectors, host cells, methods for detecting the polynocleotides, methods of screening for agents which regulate or decrease the activity of a P2Y-like GPCR protein, and a pharmaceutical composition comprising an expression vector containing a P2Y-like GPCR polynocleotide or a reagent that modulates a P2Y-like GPCR polypeptide or
                                                                                                                                       cysteinyl leukorriene receptor; cycirl LTD4; bactericide;
fungicide; protozoacide; virucide; analgesic; cytostatic; anabolic;
antiasthmatic; antiparkinsonian; cardiant; hypertensive;
hypotensive; osteopathic; antiulcer; immunosuppressive;
                                                                                                                                                                                                                                                            antiallergic; antisclerotic; neuroprotective; antipsychotic;
                                                                                                                  P2Y-like; G-protein coupled receptor; GPCR; human;
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/note= "transmembrane domain 7"
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                                                          Human P2Y-like GPCR protein,
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/label= TM1
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                                                                                                                                                                                                                                                                                              therapy; vaccine.
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                                                                                                                                                                                                                                                                                            MENLAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
         the activity of a P27-like GPCR in a disease, especially a bacterial, fungal, protozoan or viral infection, pain, cancer, anorexia, bullamia, chronic obstructive pulmonary disease, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcer, allergy, multiple sclerosis, benign prostatic hypertrophy, a psycholic disorder, neurological disorder and dyskinesia (all claimed).
The pharmaceutical composition is used to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor; GPCRX; GPCRIa; cardiomyopathy; atherosolaroas; hypertension; congenital heart defect; anorexia; atrial septal defect; ventricular septal defect; valve disease; soleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS; congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer; haemophila; idiopathic thrombocytopenic purpura; dyslipidaemia; acquired immune deficiency syndrome; diabetes; infectious disease; metabolic syndrome X; Albright Hareditary Osteodystrophy; ASD; VSD; neurodegenerative disorder; Alcheimer's disease; immune disorder; fertility; Parkinson's disorder; haematopoletic disorder;
                                                                                                                                                                                                       0;
                                                                                                                                                                           DB 22; Length 346;
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/label= Mature_human_GPCRla_protein_variant
                                                                                                                                                                                                       Indels
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                                                                                                                                                                       Score 1712; DB 22;
Pred. No. 5.8e-177;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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/label= Signal_peptide
60..346
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                                                                                                                                                                        100.08;
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                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 330; Conservative
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polynucleotide
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crown sequences are used to treat or prevent a number surject of trom GPCRX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, discuss arteriosis, pulmonary stenosis, subactic stenosis, ventricular septal defect.

(VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adenoleucodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, fertility, heamophilia, hyperoaquiation, idiopathic thrombocytopenic purpura, graft versus host disease, acquired immune deficiency syndrome (TADS), bronchial asthma, Crohn's disease, multiple sclerosis, and treatment of Albright Hereditary Osteodystrophy. GPCRX antibodies are used to treat a pathological state and treat or prevent disorders are used albabetes, metabolic disturbances associated with obesity, metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, infectious disease, cancer associated cachexia, cancer, immune disorders, haematopoietic discusse, parkinson's disorder, immune disorders, haematopoietic discusse, per therapy. The present cypishipidaemias. GPCRX DNA is also useful in gene therapy. The present cypishipidaemias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human G-protein coupled receptor proteins 1- (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for treating or preventing, e.g., cardiomyopathy, atherosclerosis, hypertension, acquired immune deficiency syndrome, bronchial asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tchernev VT, Mishra VS;
Li L, Spytek KA, Andrew DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 5.8e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crohn's disease, and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vernet CAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 6; 135pp; English.
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2000US-0183191.
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2000US-0219758.
                                                            2000US-0180929
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2001WO-US04404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Burgess CE,
Ballinger R,
                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-497077/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-497077,
N-PSDB; AAD13709
08-FEB-2001;
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Ps;
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                                                                                                                                                                                                                                                                                                                                                                             137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 196
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                                                                                                                                                                                                                                                                        MENLAISDELFISTEPFRADYYERGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVESVVR
                                                                                                                                                                                                                                                                                            KLQTMNYIALVVGCLLPFFTLSICXLLITRVLLKVEVPESGLRVSHRKALTTIITLIIF
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                                                                                                                                                                                                                                                                                                                                           FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSBQNGSVTSCLEDNLYKIA
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                                                                                                                                                                                                                                    MEPNGTESNNNSRNCTIENFKREFFPIVYLIIFFWGVI,GNGLSIYVFLQPYKKSTSVNVF
                                                                                                                                                                                                                                                                                                                                                                                                                   KLQTMNY LALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF
                                                                                                                                                                Gaps
Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                ;
0
                                                                                                                            Length 346;
                                                                                                                                                                Indels
                                                                                                                            DB 22;
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0
                                                                                                                          Score 1712; DB 22;
Pred. No. 5.8e-177;
Mismatches 0;
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                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514666/56.
                                                                                                                                               Similarity
                                                                                            346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS10778
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                                                                                                                                                              Matches 330;
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                                                                                            Sequence
                                                                                                                              Query Match
                                                                                                                                               Best Local
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                                 FLCFLPYHTLRIVHLTIWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                          FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a human G-protein coupled receptor (GPCR), hRUP14. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer.
197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITTLIIF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                             coupled receptor; GPCR; hRUP14; agonist;
                                                                                                         KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                            KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor, hRUF14.
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                                                                                                                                                                                                                                  AAU04368 standard; Protein; 346 AA
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200005-0226760.
200005-0235418.
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990S-0166099.
990S-0166369.
990S-0171900.
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2000US-0203630.
2000US-0210741.
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2000US-0242332.
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2000US-0189258.
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2000US-0196078.
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                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-355616/37.
                                                                                                                                                                                                                                                                                                                                                                             G-protein
                                                                                                                                                                                                                                                                                                                                                                                                inverse agonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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14-MAR-2000;
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10-APR-2000;
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28-APR-2000;
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12-JUN-2000;
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21-AUG-2000;
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23-DEC-1999;
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                                                 The sequence represents the amino acid sequence of cysteinyl leukotriene receptor polypeptide, termed as HIPHUM000007. The nucleic acid is useful for identifying a substance that modulates systeinyl leukotriene receptor activity. This substance is useful for treating a subject having a disorder which is responsive to cysteinyl leukotriene receptor modulation, such as asthma, chronic obstructive pulmonary disease (COPD), allergic rhinitis, cardiac arrhythmia, myocardial isohaemia, atherosclerosis and heart failure. It is also useful in the therapeutic treatment and/or prophylaxis of disorders such as acquired immune cardiency syndrome (ADDS), rhemmatoid arthritis, multiple sclerosis, leukaemia, myasthenia gravis, grave's disease, systemic lupus erythomatosus, inflammatory bowel disease, encephalomyelitis, psoriasis, erythomatosus, inflammatory bowel disease, encephalomyelitis, psoriasis, erythomatosus, inflammatory bowel disease, encephalomyelitis, psoriasis, or the antibody to cysteinyl leukotriene receptor is useful for immunoprecipitation techniques, as tools to further alucidate the function of HIPHUM000007 or its variant, and as therapeutic agent. The nucleic acid is useful for identifying mutations in HIPHUM000007 gene implicated in human disorders, which is in turn useful for disquosing the disorder or susceptibility to the disorder and in assessing the physiology of the disorders. It is also useful in hybridisation studies to monitor up- or down-regulation of HIPHUM000007 expression.
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immune deficiency and disorder
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0
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1712; DB 22; Length 346; 100.0%; Pred. No. 5.8e-177;
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allergic rhinitis,
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                           Claim 1; Page 47-48; 52pp;
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330; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               346 AA;
 lung diseases,
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Matches 330
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                                                                                                                                                                                                                                                                                                      such
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a novel human, pig and rat leukotriene C4 receptor. These sequences can be used to screen for substances that can be used in the treatment and prevention of allergic and inflammatory disorders including dermatitis, inflammatory bowel disease, ulcerative colitis, asthma and bronchitis. The present sequence is the human LTC4 receptor.
                                                                                                                                                                                                                                                                   binding activity for treating allergic and inflammatory disorders, suc as ulcerative colitis and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 MEPNGTESNNNSRNCTIENFKREFFDIVILIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
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Pred. No. 5.8e-177;
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                                                                                                                                                   Matsumoto M,
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                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 63-64; 83pp; Japanese.
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13-SEP-2000; 2000WO-JP06265.
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                                                                                                                                                                        Nishikawa T,
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Best Local Similarity
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                                          14-SEP-1999;
                                                                                                                                              Takasaki J,
                                                                                                                                                                        Isogai T,
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(first entry)

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Human; inflammatory condition, shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; peridodnata disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human novel polynucleotides and associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 582-583; 672pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-2001; 2001WO-US47004.
                                                                                       Human novel polypeptide #19.
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Yamazaki V, Ujwal ML,
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                                                                                                                                                                                                                                                                                                                     fungal infection
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                                                                                                                                                                                                                                                                                                                                                                  Homo saplens.
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ABG66684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABZ42870-ABZ42316) and/or GPCR proteins (ABP95596-ABP959942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene
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Pred. No. 5.8e-177;
0; Mismatches 0;
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2001JP-0034434.
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                                             WO200216548-A2.
Homo sapiens,
                                                                                                                                                                               04-AUG-2000;
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Matches 330;
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Wang

Wang J,

Asundi V,

Zhou P, RT;

Liu C, 1 Drmanac B

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treating inflammatory conditions such as arthritis, nephritis, Crohn's creating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischeamia-repertiation inflam, such as arthritis, nephritis, Crohn's and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral existinson's disease. Huntington's disease and amyotrophic lateral corporation of heamquopiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, esquences and platelet disorders such as thrombocytopenia, celemetric of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of estendon. In an expensive the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders infections, autoimmune disorders est multiple sclerosis and myasthenia gravis, allergic conditions such as as a myasthenia and coagulation disorders. Sequences ABG6666-ABG666758 represent human and coagulation disorders.
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/note= "Transmembrane helix"
156..173
/note= "Transmembrane helix"
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hte= "GPCR region"
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This sequence represents a human CysL2-like G-protein coupled receptor (GPCR) protein of the invention. The invention comprises the DNA and protein sequences of an isolated human CysL72 (cysteinylleukotriene2)-
like G protein-coupled receptor (GPCR) protein. This protein may have antibacterial, fungicide, virucide, cytostatic, anti-HIV, antianginal, hypotensive, hypotensive, osteopathic, tranquiliser, noctropic, anti-circlamanatory neuroprotective, antiparkinsonian, analgesic, cardiant, cerebroprotective, antiasthmatic, antiallergic, antiarthritic and antibits the function of the CysL72-like protein and is useful for treating CysL72-like GPCR disorders. The protein or its fragment are useful for treating disorders such as bacterial, fungal and are useful for treating disorders such as bacterial, fungal and viral infections and particularly those caused by human immunodeficiency (HIV) wirus, cancers, anorexia, bullmia, cardiovascular diseases (e.g. cute heart failure, angina, myocardial infarction), ulcers, osteoporosis, asthma, allergies, central and peripheral nervous system (c.g. arthritis and multiple solerosis). The coding sequence of CysL72-like GPCR polynucleotide is useful for coding sequence of CysL72-like GPCR polynucleotide is useful for coding sequence of CysL72-like GPCR polynucleotide is useful for more mannership and multiple solerosis). The coding sequence of CysL72-like GPCR polynucleotide is useful for more mannership and multiple solerosis) for more mannership and multiple solerosis.
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"GPCR region"
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                                                                                                                                                                                                                                       06-APR-2001; 2001WO-EP03981.
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13-DEC-2000; 2000US-254876P.
    /note=
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N-PSDB; AAS16243.
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antiallergic; osteopathic; cardiovascular; immunosuppressive; neoplastic; gene therapy; heart disease; gastrointestinal disease; sleep disorder; immunological disorder; pulmonary disorder; infectious disease; sleep disorder; pulmonary disease; inflammatory bowel disease; myeloproliferative pulmonary disease; inflammatory bowel disease; diabetes; metabolic disease; neurological disease; urogenital disease; inflammation; cancer; osteoporosis; cardiovascular disease; infection; anlergy, respiratory disease; sensory organ disorder; hair loss; immunological disorder; pulmonary disease; neoplastic disease; vasculitic granulomatous disease; dermatology; psychotherapeutic.
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vascular disorders, reproductive diseases, or diseases related to cellular metabolisam, growth, development, blood and bone homeostasis. These disorders or diseases include asthma, inflammation, allergy, angiogenesis, respiratory distress syndrome, crohn's disease, oedema, high or Low blood pressure growth, development, blood and bone homeostasis. Human CysLT2 GPCR is also used in protein therapy. The present sequence is human CysLT2 GPCR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; G-protein coupled receptor; GPCR; PFI-017*; cytostatic;
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                          FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human CySLT2 GPCR (G-protein coupled receptor) polypeptide and its corresponding nucleic acid. The human CySLT2 GPCR, antibodies and compositions are useful for treating the human or animal body, or for diagnosing a disease. Human CySLT2 GPCR is useful for diagnosing, preventing and treating inflammatory, immunological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New HUMAN CysLT2 GPCR (G-protein coupled receptor), useful for diagnosing, preventing and treating inflammatory, immunological or vascular disorders, e.g. asthma, allergy, angiogenesis, Crohn's disease
    Human, CysLT2 GPCR; G-protein coupled receptor; oedema; asthma; immunological disorder; vascular disorder; reproductive disease; cellular metabolism; growth; development; blood; bone homeostasis; inflammation; allergy; angiogenesis; respiratory distress syndrome; crohn's disease; blood pressure; protein therapy; anti-inflammatory; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Extracellular domain between the second and third transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Extracellular domain between the fourth and fifth transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Extracellular domain between the sixth and
                                                                                                                                                                                                                                                                                                                                                Human CysLT2 GPCR (G-protein coupled receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seventh transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-glycosylation site"
268..289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Extracellular_domain
                                                                                         317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                   KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                     AAE17231 standard; Protein; 346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1A-1C; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001; 2001WO-US16965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-207725P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26..28
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-154523/20.
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                                                                                                                                                                                                                                                               AAE17231;
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                          257
                                                                   301
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                                                                                                                                                                          RESULT 14
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240

Harland L;

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The sequence represents a novel G-protein coupled receptor (GPCR),
PRI-017* of the invention. The PRI-017 has cytostatic, antiallergic,
Csteopathic, cardiovascular, and immunosuppressive activity. The
csteopathic, cardiovascular, and immunosuppressive activity. The
polynucleotides may have a use in gene therapy. The polynucleotide is
useful for treating allergic disorders, an inflammatory disorder, an
immological disorder, a pulmonary disorder, an infectious disease, a
meoplastic or myeloproliferative disease, or a heart disease. The
cmeoplastic or myeloproliferative disease, or a schma, the pulmonary
disease. PRI-017 polynucleotide sequences may be used for the disquosis
clisease. PRI-017 polynucleotide sequences may be used for the disquosis
of diseases resulting from expression of PFI-017, and to detect and
quantify gene expression in conditions, disorders or diseases in which
cquantify gene expression in conditions, disorders or diseases in which
cpri-017 activity may be implicated. The polypeptides are used to produce
anti-PRI-017 activity may be implicated. The polypeptides are used to produce
cc pri-017 activity may be implicated. The polypeptides are used to produce
compositions which can modulate the pelyfide can be used in treating
compositions which can modulate the peptide can be used in treating
compositions which can modulate the peptide can be used in treating
casse, inflammation, cancer, osteoporosis, cardiovascular disease,
cantontestinal disease, infections, allery and respiratory disease,
sensory organ disorders, sleep disorders, hair loss, immunological
cmyconferative diseases, vascultic granniomatous diseases, and heart
compositions which diseases, used in dermatology, and psychotherapeutics.
                                                                                                                                                                     New PFI-017 protein and polynucleotide encoding the protein, useful for diagnosing or treating metabolic diseases, urogenital disease, immunological disorders, infectious diseases, neoplastic or myeloproliferative diseases
                                                                                                                                                                                                                                                                                                                                 Claim 7; Fig 7B; 39pp; English.
                                                                                          WPI; 2002-040722/05.
N-PSDB; AAH77279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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61 MINIFAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVR 120 121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180 181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALFTIITTLIIF 240 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLXYFAGENFKDRL 300 9 17 MEPNGIFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFIQPYKKSTSVNVF 76 1 MEPNCIPSNNNSRNCTIENFKREFFPIVYLIIFFWGYLGNGLSIYVFLQPYKKSTSVNVF 0; Gaps 100.0%; Score 1712; DB 23; Length 346; 100.0%; Pred. No. 5.8e-177; Live 0; Mismatches 0; Indels 0; 301 KSALRKGHPOKAKTKCVFPVSVWLRKETRV 330 Query Match
Best Local Similarity 100.0
Matches 330; Conservative 셤 g δ á qq ΩŽ g δğ g δŽ δ

Search completed: October 8, 2003, 08:32:03 Job time: 87 secs

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October 8, 2003, 08:26:59; Search time 40 Seconds (without alignments) 793.392 Million cell updates/sec
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1712
1 MEPNGTFSNNNSRNCTIENF...........KAKTKCVFPVSVWLKKETRV 330
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	G protein-coupled	G protein-coupled	G protein-coupled	P2Y receptor - bov	G protein-coupled	intron 17 puriners	heptahelical P2Y5-	ATP receptor P2u -	platelet-activatin	P-2U nucleotide re	platelet-activatin	thrombin receptor	platelet activatin	proteinase-activat	angiotensin recept	platelet-activatin	chemokine (C-C) re	G protein-coupled	macrophage inflamm	proteinase activat	probable chemoattr	G protein-coupled	lymphocyte-specifi	G protein-coupled	MIP-1 alpha recept	G protein-coupled	somatostatin recep	somatostatin recep	G protein-coupled
SUMMARIES	II	S33733	I50241	JC4737	JC4162	B45680	T09508	JC5549	A47556	S13638	A54946	A40191	151667	863666	S66518	I38435	\$43252	A45177	I55450	I49339	148705	JC5796	JC5498	B55735	JC5067	I49340	I69202	157955	JN0763	A55735
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o N P	Query Match	27.3	26.1	26.1	25.8	25.7	25.5	25.1	24.4	24.3	24,3	23.9	23.6	23.6		23.5	23.2	23.0	22.8	22.8	22.8			22.1				21.8		
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RESULT 2
150241
6 protein-coupled receptor 6H1 - chicken N;Alternate names: purinoceptor 6H1 C;Species: Gallus gallus (chicken)

somatostatin recep	G protein-coupled	G protein-coupled	G protein-coupled	chemokine (C-C) re	alpha-thrombin rec	angiotensin II rec	angiotensin II rec	chemokine (C-C) re	thrombin receptor	P2Y6 receptor - hu	G protein-coupled	G protein-coupled	G protein-coupled	angiotensin II rec	angiotensin II rec
I57940	S68208	S55594	568679	G02436	S17148	JN0694	S15403	A43113	A43448	JC4800	I65989	JC5653	A45680	A48857	A49092
~	~	N	~	C)	~	7	C4	(7)	~	7	7	7	7	7	7
363	365	383	365	355	427	362	359	352	432	328	333	361	378	359	363
21.7	21.7	21.6	21.6	21.4	21.4	21.3	21.2	21.1	21.0	20.9	20.8	20.8	20.8	20.8	20.8
		'n	0,	366	366	364.5	363	361.5	360	357	6.5	356.5	5.5	356	356
372	371.5	370.	æ	m	(**)	36		36			3	35	35		

ALIGNMENTS

B.F.; Burr FP receptor	7;	62 80	122	173 199	233 251	287 311	
RESULT 1 S33733 G protein-coupled receptor - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: O-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999 C;Accession: S33733 R;Mebb, T.E.: Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.E.FEBS Lett. 324, 219-225, 1993 A;Title: Cloning and functional expression of a brain G-protein-coupled ATP 1A;Reference number: S33733 A;Accession: S33733 A;Accession: S33733 A;Accession: S33733 A;Accession: S33733 A;Accession: S33733 A;Colecule type: mRNA A;Residues: 1-362 <webs- a;colecule="" mrna="" td="" ty<="" type:=""><td>Query Match 27.3%; Score 467; DB 2; Length 362; Best Local Similarity 30.7%; Pred. No. 1.3e-31; Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps</td><td>QY 5 GTFSHNNSRNCT1ENPKREPPIVYLIIFFWGVLGNGLSIYVFLQPYXKSTSVNVFML 6: : : : </td><td>QY 63 NLAISDLÆISTLÆFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYELTVLSŸVRFL 1: :: :: : : : Db 81 NLALADFLYVLTLPALIFYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYT 1:</td><td>OY 123 AMYHPERLLHUTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLE I. </td><td>QY 174 INLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLIKVEVPESGLRVSHRKALTTI 2:</td><td>QY 234 IITLIFFLGFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPL 28 </td><td>QY 288 IXYFAGENFKDRLKSALRK 306 : : : </td></webs->	Query Match 27.3%; Score 467; DB 2; Length 362; Best Local Similarity 30.7%; Pred. No. 1.3e-31; Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps	QY 5 GTFSHNNSRNCT1ENPKREPPIVYLIIFFWGVLGNGLSIYVFLQPYXKSTSVNVFML 6: : : :	QY 63 NLAISDLÆISTLÆFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYELTVLSŸVRFL 1: :: :: : : : Db 81 NLALADFLYVLTLPALIFYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYT 1:	OY 123 AMYHPERLLHUTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLE I.	QY 174 INLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLIKVEVPESGLRVSHRKALTTI 2:	QY 234 IITLIFFLGFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPL 28	QY 288 IXYFAGENFKDRLKSALRK 306 : : :

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A Map position: 3pter-3qter

(5.Superfamily: Aftr acceptor P2u

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(5.Superfamily: Acceptor P2
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C;Comment: This receptor belongs to a family of G protein-coupled receptors. It respondencies:
   R:Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, Blochem. Blophys. Res. Commun. 218, 783-788, 1996
A:fitle: Cloning and chromosomal localization of the human P2XI purinoceptor. A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615; MUID:96158962; PMID:8579591
A;Molecule type: mRRA
A;Molecule type: mRRA
A;Residues: 1-373 <AXY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVRFLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE----L 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 NLYKIAKLQIMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALITII 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 RSYFIYSWCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2T receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-0ct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C;Accession: JG4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TFSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLIIFFLCFLPYHTLRTVHLTT - - - - WKVGLC - - KDRLHKALVITLALAAANACFNPLL
                                                                                                                                                                                                                                                           A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 446; DB 2; Length 373
Pred. No. 7.5e-30;
9; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                              R.Leon, C.; Vial, C.; Cazenave, J.; Gachet, C. submitted to the EMBL Data Library, May 1995
A.Description: Cloning of a human putative P2X receptor. A.Reference number: 554253
A.Reference number: 554253
                                                                                                                                                                                                                                                                  A; Cross-references: GDB:677125; OMIM:601167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.1%; Scc
lilarity 32.1%; Pre
Conservative 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
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les 102; Conserv
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                  C. Accession: 150241; J05618

R; Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 638-636, 199

R; Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 638-636, 199

A; Title: Identification of a G protein coupled receptor induced in activated T cells.
A; Reference number: 150241; MUID: 93329058; PMID: 8393036

A; Recession: 150241

A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1508 (*ME)
A; Cross-references: GB: L06109; NID: 9304383; PIDN: AAB06587.1; PID: 9304384
R; Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A; Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A; Reference number: JC4618; MUID: 96190677; PMID: 8619790
A; Residues: 1-308 (*WEb>
A; Mescaleus: 1-308 (*WEb>
A; Mescaleus: T-cells
A; Mescaleus: T-cells
C; Comment: This receptor plays a role in T-cell activation.
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Nyllernate names: P2XI purinergic receptor; P2XI purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
C;Accession: JC4737; JC4615; S54253
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A;Title: Cloning and tissue distribution of the human P271 receptor. A;Reference number: JC4737; MJD:96205320; PMID:8630005
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-373 < JANA
A;Residues: 1-373 < JANA
A;Cross-references: GB:S81950; NID:91839438; PIDN:AAB47091.1; PID:91839439
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C;Superfamily: ATP receptor P2u

C;Superfamily: ATP receptor P2u

C;Reywords: G protein-coupled receptor; transmembrane protein

F;15-40/Domain: transmembrane #status predicted <TM1>

F;91-74/Domain: transmembrane #status predicted <TM2>

F;89-109/Domain: transmembrane #status predicted <TM3>

F;137-23/Domain: transmembrane #status predicted <TM4>

F;177-201/Domain: transmembrane #status predicted <TM5>

F;277-248/Domain: transmembrane #status predicted <TM5>

F;269-292/Domain: transmembrane #status predicted <TM5>
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C; Species: Homo sapies (man)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C; Accession: T09508
R; Bohm, S:K:; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W. submitted to the EMBL Data Library, April 1997
A; Description: The human purinergic receptor P275 is encoded in intron 17 of A; Accession: T09508
A; Accession: T09508
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           Gaps
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           18;
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C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                Indels
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           135;
                Mismatches
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           63;
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Best Local Similarity 32.03
Matches 98; Conservative
           Conservative
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           102;
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F:52-77/Domain: transmembrane #status predicted <TML>
F:88-111/Domain: transmembrane #status predicted <TML>
F:14-150/Domain: transmembrane #status predicted <TML>
F:14-150/Domain: transmembrane #status predicted <TML>
F:14-130/Domain: transmembrane #status predicted <TML>
F:214-230/Domain: transmembrane #status predicted <TML>
F:214-237/Domain: transmembrane #status predicted <TML>
F:36-382/Domain: transmembrane #status predicted <TMC>
F:305-328/Domain: transmembrane #status predicted <TMC>
F:305-328/Domain: transmembrane #status predicted <TMC>
F:311,27,113,197/Binding site: carbohydrate (Asn) (covalent) (by protein kinase A) #status predicted F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
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C; Species: Homo saplens (man)
C; Date: 21-569-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: B4580
R; Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
T; Yizol. 67, 2209-2220, 1993
A; Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled A; Reference number: A45680; MUID:93188173; PMID:8383238
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                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residuss: 1-373 <hr/>-HEN>
A;Cross-references: BMB:X87628; NID:gl032484; PIDN:CAA60958.1; PID:gl032485
A;Experimental source: aortic endothelial cell
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C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
E:52-77/Domain: transmembrane #status predicted <TML>
F;88-111/Domain: transmembrane #status predicted <TM2>
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A) Molecule type: nucleic acid
A) Residues: 1-361 - BIR>
A) Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057
A) Experimental source: B-1ymphocytes
A; Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIP:127097)
C; Superfamily: ATP receptor P2u
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Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A; Title: Cloning and characterisation of a bovine P2Y receptor. A; Reference number: JC4162; MUID:95352058; PMID:7626079
A; Accession: JC4162
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Pred. No. 2.3e-29;
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Best Local Similarity 31.0°
Matches 95; Conservative
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Db 5 LEPWNSTINGTWEGDELGYRCRFNEDFRYVLLPVSYGVVCVLGLCINVVALYIFLCRLKT 64 Qy 54 STSVNVFMLNIAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 113	STATEMENT OF THE STATEM	OY 282 ACRIPLINIA SALAKUSHPAKAN 314 1 1:1; 1 1 1 299 SCLDPVLYFLAGORLVRFARDARPPTEPT 327 RESULT 9 S13638 platelet-activating factor receptor - quinea pig C; Species: Cavia porcellus (quinea pig) C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999 C; Accession: S13638 R; Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H. Nature 349, 342-346, 1991	A; Title: Cloning by functional expression of platelet-activating factor receptor from A; Reference number: \$13638; MUID:91101726; PMID:1846231 A; Accession: \$13638 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-342 < HOD. A; Cross-references: \$GB:X56736; NID:949442; PIDN:ChA40060.1; PID:949443 A; Note: the species of guinea pig is not identified; in GenBank entry CCPAPREC, released; Superfamily: ATP receptor P2u Query Watch 24.3%; Score 416; DB 2; Length 342; Best Local Similarity 30.4%; Pred. No. 2.2e-27; Assistant Application of the content of the conte	11 NSRNCTIENEKREFEPIVYLIIFEWGVLGNGLSIYVFLQPYKKSTSVNVFMLALAISD 68 1 NSRNCTIENEKREFEPIVYLIIFEWGVLGNGLSIYVFLQPYKKSTSVNVFMLALAISD 68 1	129 RLHHYTSIRSAWILCGIIWILIMASSIMLLDSGSEGNGSYTSCLELNLYKIAK	302 KHLSEKLNIMRSSQKC 302 KHLSEKLNIMRSSQKC 3946 20 nucleotide receptor - human
: :: Db 298 IQNSIK 303	RESULT 7 Deptabelical P2Y5-like receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: JG5549 R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. R;Janssens, R.; Doeynaems, J.M.; Godart, M.; Communi, D. R;Janssens, R.; John, Res. Commun. 2356, 106-112, 1997 A;Title: Cloning of a human heptabelical receptor closely related to the P2Y5 receptor A;Reference number: JG5549 A;Accession: JG549 A;Accession: JG5549 A;Accession: JG5549 A;Accession: JG5549 A;Accession: JG5549 A;Accession: JG5549 A;Accession: JG5549	Query Match 25.1%; Score 430; DB 2; Length 370; Best Local Similarity 31.7%; Pred. No. 1.6e-28; Matches 103; Conservative 70; Mismatches 132; Indels 20; Gaps 9; QY 5 GTFSNNNSRNCTI-ENFKREFFPIVYLIFFWGVLGNGLSIYVFLOPYKKSTSVNVFMLN 63	124 MVHPFRLIHVTSIRSAWILCGIIWILIMASSIML-LDSGSEQNGSVTSCLEINLYKIAK- 181	QY 297 KDRLKSALRKGHPQKAK 313 ::	C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 13-3dan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999 C;Accession: A47556 R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells. A;Reference number: A47556; MuID:93281707; PMID:7685114 A;Accession: A47556 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-373 <lus> A;Cross-references: GB:114751; NID:9309457; PIDN:AAA39871.1; PID:9309458 C;Superfamily: ATP receptor P2u C;Superfamily: ATP receptor P2u C;Reywords: transmembrane protein</lus>	<pre>Query Match Best Local Similarity 31.8%; Pred. No. 1.5e-27; Matches 106; Conservative 67; Mismatches 131; Indels 29; Gaps 10; Oy 1 MEPNOTESNNN-SRNCTI-ENFREFFPIVYLIIFFWGYLGNGLSIYVFLOPYKK 53 : : </pre>

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A.Fesidues: 1315, W. 317-342 <SUG>
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A.Fesidues: 1315, W. 317-342 <SUG>
A.Fesidues: 1315, W. 317-342 <SUG>
A.Foreimental source: heart
A.Note: the authors translated the codon AAT for residue 316 as Lys
R.Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
R.Seyfried, C.E.; Schweickart, W.L.; Godiska, R.; Gray, P.W.
A.Title: The human platelet-activating factor receptor gene (PTAFR) contains no intr
A.Fecsesion: A42831
A.Molecule type: DNA
A.Residues: 1226, TG, 229-342 <SEY>
A.Cross-references: GB:M68177; NID:9190697; PIDN:AAA60214.1; PID:9190698
A.Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R.Chase, P.B.; Halonen, M.; Regan, J.W.
A.Title: Cloning of a human platelet-activating factor receptor gene: evidence for a A.Reference number: 151923; MUID:93192035; PMID:8383507
                                                                                                                                                                                                                                          A) Molecule type: mRNA
A) Residues: 1-342 < NAKA
A) Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976
A) Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976
B) Cohem. Biophys. Res. Commun. 189, 617 624, 1992
A) Title: Molecular cloning and characterization of the platelet-activating factor re
A) Reference number: JC1359; MUID:93112021; PMID:1281995
                                                      A;Title: Molecular cloning and expression of platelet-activating factor receptor fro A;Reference number: A41079, MUID:92041873; PMID:1657923 A;Accession: A41079 A;Status: not compared with conceptual translation
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A;Molecule type: DNA
A;Residues: 1-342 <RES>
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A;Cross-references: GDB:128806; OMIM:173393
              Chem. 266, 20400-20405, 1991
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C; Superfamily: ATP receptor P2u
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F;233-253/Domain:
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                                                                                    Chacessian: A54946

R:Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Scil. U.S.A. 91, 3275-3279, 1994

A:Title: Clouing and expression of a human P-20 nuclectide receptor, a target for cystic A:Reference number: A54946; MUID:94211846; PMID:8159738

A:Status: preliminary protein

A:Residues: 1-375 < PAR>
A:Cross-references: GB:U07225

A:Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
A:Genetics:

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A;Residues: 1-342 <YERS
A;Cross-references: GB:M80436; NID:g189537; PIDN;AAA60001.1; PID:g189538
A;Cross-references: GB:M80436; NID:g189537; PIDN;AAA60001.1; PID:g189538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka; C.; Mutoh, H.; Minami, M.; Bito, H.; Sey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LQTMNYIALVVGCL--LPFFTLSICYLLIRVLLKVEVPES-GLRVSHRKALTTIITLI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLA----LAAANACFNPLLYYFAG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
:Species: Homo sapiens (man)
Date: 11-Nov-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 NGTFSNNN-SRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 NGTWDGDELGYRCRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 INLAISDELFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF
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A; Residues: 1-342 (RUNA)
A; Cross-references: CB:M76674; NID:9456293; PIDN:AAA60002.1; PID:9456294
R; Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biocham: Biocham: Brophys. Res. Commun. 180, 105-111, 1991
A; Title: Characterization of a human cDNA that encodes a functional recept A; Reference number: JH0479; MUID:92028922; PMID:1656963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.4e-27;
67; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 416; DB 2;
Pred. No. 2.4e-27;
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31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.6%
Matches 100; Conservative
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C;Species: Homo sapiens (man)
C;Cibate: 28-Oct.1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: $66518; $64709; $90211.
R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A;Title: Molecular cloning and functional expression of the gene encoding the human paracession: $66518; MuID:96048032; PMID:7556175
A;Accession: $66518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Cross-references: EMBL: Z49993; NID:91008084; PIDN:CAA90290.1; PID:91008085
R/Bochm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; R
Biochem, J. 314, 1009-1016, 1996
A/Title: Molecular cloning, expression and potential functions of the human proteinas
A/Reference number: S64709; MUID:96177879; PMID:8615752
A/Accession: S64709
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                                                           VFMINIAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
                                                                                                         LE-LNLYKIAKLQTMNYIALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTTIIITLIIFELCELPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFN 285
                                                                                                                                                                                              119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGS------EQNGSVTSC 171
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1 MEHNGSFRVDS-----EFRYTLFPIVYSVIFILGVVANGYVLWVFANLYPSKKLNEIK 53
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A;Residues: 29-397 <KAH>
A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
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F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted <WAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVIYCFLTKKFRKHLS---EKFYSMRSSRKC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
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A;Molecule type: DNA
A;Residues: 1-397 <NYS>
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                                                                                                                                                                                                                                               C.Species: Xenopus lacvis (African claved frog)
C.Date: 13-5ep-1996 #sequence_revision 13-5ep-1996 #text_change 21-Jul-2000
C.Date: 151667
S.Geression: 151667
Nature 368, 648-651, 1994
A.Title: Thrombin receptor's specificity for agonist peptide is determined by its extract A.R.Reference number: 151667; MUID: 94195429; PMID: 8145852
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C; Species: Mus musculus (house mouse)
C; Date: 28-oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: S63666
R; Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
Biochem. J. 314, 671-678, 1996
A; Title: A murine platelet-activating factor receptor gene: cloning, chromosomal lo
A; Reference number: S63666; MuID:96239129; PMID:8670084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 FYIYYESSF--CLLFPFVPFIITICYIGIIRSLSSSSIENS---CKKTRALELAVVVLC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 HPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ---NGSVTSCLELNLYKIAKL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 QTMNYIALVVGCLL----PFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEPNGIFSNNNSRNCTIENFKREFFPIVYLIIFFWGYLGNGLSIYVF--LQPYKKSTSVN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 RNCTIE-----NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g495198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.6%; Score 404.5; DB 2;
32.4%; Pred. No. 2.5e-26;
tive 61; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                   LYYFAGENFKDRLKSALRKGHPQKAKTKC 316
                                                                                                                                                                                                                          thrombin receptor - African clawed frog
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Best Local Similarity 30.55
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 YLYSLL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLKSAL 304
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Matches 99; Conserv
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A;Molecule type: DNA
A;Residues: 1-341 <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-420 <GE
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288
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A,Title: A human gene that shows identity with the gene encoding the angiotensin receptor A,Reference number: 138435, MUID:94124031; PMID:8294032
A,Rocession: 138435
A;Status: preliminary
A,Molecule type: DNA
A,Residues: 1-380 <RES>
A;Cross-references: EMBL:U03642; NID:9425351; PIDN:AAA18954.1; PID:9425352
                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiotensin receptor homolog APJ - human
C;Species: Homo sapiens (man)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
R;Orcession: 138435
R;Orbowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                          189 ALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCPLPY 247
                                                                                                                                                                    304 NLLLVVHYFLIK-SQGQSHVYALYIVALCLSTINSCIDPFVYYFVSHDFRDHAKNALL-- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWIL--IMASSIMLL-DSGSEQNGSVTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 CLELNLYKIAKLQT-----KVEV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 273
144 GI---IWILIMASSIML------LDSGSEQNGSVTSCLEINLYKIAKLQTMNY-I 188
                                                                                                                                                                                                                               248 HTLRTVHLITWKVGLCKDRLHRALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 PYCTCISYVNSCINPFLYAFFDPRFRQACTSMLCCGQSRCAGT 334
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                                                                                                                                                                                                                                                                                                              308 HPQKAKTKCVFPVSVWLRKETR 329
                                                                                                                                                                                                                                                                                                                                           361 -CRSVRTVKQMQVSLTSKKHSR 381
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A,Map position: 11q12
A,Introns: #status absent
C,Superfamily: vertebrate rhodopsin
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